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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:10:25 ; Search time 33.5 seconds
(without alignments)
871.180 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLSYSEVLPNPKVQEHYNY.....LRCGMHPTPTFLEGNTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
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5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1809	100.0	353	2	US-09-582-200A-4
2	1809	100.0	353	2	US-09-582-200A-6
3	1809	100.0	353	2	US-09-582-200A-12
4	1809	100.0	353	2	US-09-731-030A-19
5	1803	99.7	353	2	US-09-582-200A-2
6	1803	99.7	353	2	US-09-582-200A-5
7	1803	99.7	353	2	US-09-582-200A-10
8	1760	97.3	353	2	US-09-274-752D-3
9	1625.5	89.9	352	1	US-08-196-989B-2
10	1625.5	89.9	352	1	US-08-760-936-2
11	1625.5	89.9	352	2	US-09-582-200A-11
12	1625.5	89.9	352	2	US-09-169-205D-24
13	1625.5	89.9	352	2	US-09-225-024-2
14	849	46.8	383	1	US-08-262-477-2
15	847	46.8	383	1	US-08-196-989B-4
16	847	46.8	383	1	US-08-760-936-4
17	847	46.8	383	2	US-09-225-024-4
18	845	46.7	382	2	US-09-542-733-2
19	836.5	46.2	381	1	US-08-845-566-3
20	836.5	46.2	381	1	US-08-467-948A-28
21	836.5	46.2	381	2	US-08-852-824-18
22	836.5	46.2	381	2	US-08-467-947A-28
23	836.5	46.2	381	2	US-09-731-030A-17
24	836.5	46.2	381	4	PCT-US96-10618-4
25	836.5	46.2	381	4	PCT-US96-10618-4
26	831	45.9	382	2	US-09-169-205D-21
27	769	42.5	378	2	US-09-082-088-2

28	769	42.5	378	2	US-09-546-117-2	Sequence 2, Appli
29	769	42.5	378	2	US-09-169-205D-22	Sequence 22, Appl
30	769	42.5	378	2	US-09-731-030A-18	Sequence 18, Appl
31	763	42.2	334	1	US-08-118-270-73	Sequence 73, Appl
32	763	42.2	334	4	PCT-US93-08528-73	Sequence 73, Appl
33	720.5	39.8	500	2	US-09-875-076-30	Sequence 30, Appl
34	535	29.6	384	2	US-09-731-030A-11	Sequence 11, Appl
35	531	29.4	384	2	US-09-731-030A-13	Sequence 13, Appl
36	523	28.9	384	2	US-08-852-824-4	Sequence 4, Appli
37	523	28.9	384	2	US-09-518-383-4	Sequence 4, Appli
38	515	28.5	393	4	PCT-US96-10618-3	Sequence 3, Appli
39	512	28.3	364	2	US-09-169-205D-20	Sequence 20, Appl
40	511	28.2	364	2	US-08-763-938-2	Sequence 2, Appli
41	509	28.1	364	4	PCT-US96-10618-2	Sequence 2, Appli
42	506	28.0	364	2	US-09-731-030A-15	Sequence 15, Appl
43	506	28.0	364	2	US-09-811-838-2	Sequence 2, Appli
44	492	27.2	382	2	US-09-169-205D-23	Sequence 23, Appl
45	492	27.2	382	2	US-09-274-752D-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-582-200A-4
; Sequence 4, Application US/09582200A
; Patent No. 6482609

GENERAL INFORMATION:

; APPLICANT: Munroe, Donald G.

; APPLICANT: Kamboj, Rajender

; APPLICANT: Peters, Diana

; APPLICANT: Kooshesh, Fatemeh

; APPLICANT: Vyas, Tejal B.

; APPLICANT: Gupta, Ashwani

; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R

; FILE REFERENCE: 108074-00002

; CURRENT APPLICATION NUMBER: US/09/582,200A

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 09/222,995

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: PCT/CA98/01195

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 60/109,885

; PRIOR FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/080,610

; PRIOR FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: 60/070,185

; PRIOR FILING DATE: 1997-12-30

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-582-200A-4

Query Match 100.0%; Score 1809; DB 2; Length 353;

Best Local Similarity 100.0%; Pred. No. 8.7e-146; Indels 0; Gaps 0;

Matches 353; Conservative 0; Mismatches 0;

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DB	1	MGSLSYSEVLPNPKVQEHYNYTKETLETQTTTSRQVASAFIVILCCAIVVENLLVIAVAR	60
QY	61	NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV	120
DB	61	NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV	120
QY	121	FSLLAIATERHVAIAKVKLYGDKSCRMILLIGASWLSLVGLGGLPILGNCILGHEACS	180
DB	121	FSLLAIATERHVAIAKVKLYGDKSCRMILLIGASWLSLVGLGGLPILGNCILGHEACS	180
QY	181	TVLPLVAKHYLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG	240

Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALKKTVTIVLG 240
QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGMHMTPTPTFLEGNTVV 353
Db 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGMHMTPTPTFLEGNTVV 353

RESULT 2
US-09-582-200A-6
; Sequence 6, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-200A-6
Query Match 100.0%; Score 1809; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.7e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSLYSEYLNPNKVOEHYNTKETLEQTTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNTKETLEQTTSRQVASAFIVILCCAIWENLLVLIIVAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
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Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALKKTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALKKTVTIVLG 240
QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
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Db 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGMHMTPTPTFLEGNTVV 353

RESULT 3
US-09-582-200A-12
; Sequence 12, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 #36
US-09-582-200A-12
Query Match 100.0%; Score 1809; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.7e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGSLYSEYLNPNKVOEHYNTKETLEQTTSRQVASAFIVILCCAIWENLLVLIIVAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALKKTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPOTLALKKTVTIVLG 240
QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGMHMTPTPTFLEGNTVV 353
Db 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGMHMTPTPTFLEGNTVV 353

RESULT 4
US-09-731-030A-19
; Sequence 19, Application US/09731030A
; Patent No. 6566096
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015

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; CURRENT APPLICATION NUMBER: US/09/731,030A
; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

Query Match          100.0%; Score 1809; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 8.7e-146; Indels 0; Gaps 0;
Matches 353; Conservative 0; Mismatches 0;

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DB 1 MGSLSYSEYLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAR 60
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DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLGASWLSISLVGLGPIILGWNCLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLGASWLSISLVGLGPIILGWNCLHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALKTKTVTVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALKTKTVTVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNVTV 353
DB 301 RPLQWRPGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNVTV 353

RESULT 5
US-09-582-200A-2
; Sequence 2, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CONFLICT
; LOCATION: (272)..(274)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
; FEATURE:
; NAME/KEY: misc_feature
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: Unknown Xaa refers to any amino acid
US-09-582-200A-2

Query Match          99.7%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 2.8e-145;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MGSLSYSEYLNPNKVOEHYNYTKETLETQETTSRQVASAFIVILCCAIVVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLGASWLSISLVGLGPIILGWNCLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLGASWLSISLVGLGPIILGWNCLHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALKTKTVTVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALKTKTVTVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNVTV 353
DB 301 RPLQWRPGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNVTV 353

RESULT 6
US-09-582-200A-5
; Sequence 5, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CONFLICT
; LOCATION: (272)..(274)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (273)..(273)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
US-09-582-200A-5

Query Match          99.7%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 2.8e-145;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60

QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353

RESULT 7
US-09-582-200A-10
; Sequence 10, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Koosheah, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIOR FILING DATE: 2000-07-28
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 polypeptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: "Xaa" represents any amino acid
US-09-582-200A-10

Query Match          99.7%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 2.8e-145;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60

QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353
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QY 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60

QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353

RESULT 8
US-09-274-752D-3
; Sequence 3, Application US/09274752D
; Patent No. 6812335
; GENERAL INFORMATION:
; APPLICANT: Goetzl, Edward L.
; APPLICANT: An, Songzhu
; TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipids and
; FILE REFERENCE: A-67501/DJB/TAL
; CURRENT APPLICATION NUMBER: US/09/274,752D
; CURRENT FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-274-752D-3

Query Match          97.3%; Score 1760; DB 2; Length 353;
Best Local Similarity 98.0%; Pred. No. 1.3e-141;
Matches 346; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVILCCAIVVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAGIVILCCAIVVENLLVLIIVAR 60

QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180
Db 121 GSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLGPLIGMNCGLGLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHHLLPLRSSSSSLERGMMPTSPTFLEGNTVV 353
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RESULT 11
US-09-582-200A-11
; Sequence 11, Application US/09582200A
; Patent No. 6482609

Query Match	89.9%	Score 1625.5	DB 1	Length 352
Best Local Similarity	89.5%	Pred. No. 3.3e-130		
Matches 316	Conservative 14	Mismatches 22	Indels 1	Gaps 1
Qy	1	MGSLSYSEYLPNPKVQEHYNYKTELTQETTSRQVASAFIVLCCAVVENLLVLI	AV 60	
Db	1	MGGLSYSEYLPNPKVQEHYNYKTELDQETTSRQVASAFIILCCAVVENLLVLI	AV 60	
Qy	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAF	ITLSASV 120	
Db	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPQWFAREGSAF	ITLSASV 120	
Qy	121	PSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLISLVGGPIILGNWCLGH	LEACS 180	
Db	121	PSLLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLISLIIGGPIILGNWCLGH	LEACS 180	
Qy	181	TVLPYAKHYVLCVVTTFESIILLAVVLYVRIYCVVRSSSHADMAAPOTLALK	TVTVILG 240	
Db	181	TVLPYAKHYVLCVVTTFSVILLAIIVLYVRIYFVVRSSHADVAGPOTLALK	TVTVILG 240	
Qy	241	VFIICWLPAPFSILLDDACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRS	SRDLRREV 300	
Db	241	VFIICWLPAPFSILLDDSTCPVRACPVLYKAHYFFAFATLNSLLNPVIYTW	RSDLRREV 300	
Qy	301	RPLOCWRPGVQVQRRRGTTFGHLLPLLRSSSLERGMHMPSTPTFLSGNTV	V 353	
Db	301	RPLLCWRQKGATG-RRGNPGHRLPLLRSSSLERGLHMPSTPTFLSGNTV	V 352	

```
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIORITY FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 352
; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11

Query Match      89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKQVEHYNYTKETLETTQTSRQVASAFIVILCCAIWENLLVLIAR 60
Db 1 MGSLYSEYLNPEKQVEHYNYTKETLDMQETSPKVASAFIILCCAIWENLLVLIAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSILVGLGPILGWNCLEHLEACS 180
Db 121 FSLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSILVGLGPILGWNCLEHLEACS 180

Qy 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVLPYAKHYVLCVVTIFSVILLALVALYVRIYFVVRSSHADVAGPQTLALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSTILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIIICWLPAPFSTILLDSTCPVRACPVLYKAHYFFAFATLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLOCWRPGVGQRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLLCWRQKGATG-RRGNPGHRLPLRSSSSLERGLHMTSPTFLEGNTVV 352

RESULT 13
US-09-225-024-2
; Sequence 2, Application US/09225024
; Patent No. 6518414
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,024
; FILING DATE: 04-JAN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,936
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/196,989
; FILING DATE: 15-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
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; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIORITY FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 352
; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11

Query Match      89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKQVEHYNYTKETLETTQTSRQVASAFIVILCCAIWENLLVLIAR 60
Db 1 MGSLYSEYLNPEKQVEHYNYTKETLDMQETSPKVASAFIILCCAIWENLLVLIAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSILVGLGPILGWNCLEHLEACS 180
Db 121 FSLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSILVGLGPILGWNCLEHLEACS 180

Qy 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVLPYAKHYVLCVVTIFSVILLALVALYVRIYFVVRSSHADVAGPQTLALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSTILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIIICWLPAPFSTILLDSTCPVRACPVLYKAHYFFAFATLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLOCWRPGVGQRRRGTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLLCWRQKGATG-RRGNPGHRLPLRSSSSLERGLHMTSPTFLEGNTVV 352

RESULT 12
US-09-169-205D-24
; Sequence 24, Application US/09169205D
; Patent No. 6485922
; GENERAL INFORMATION:
; APPLICANT: Erikson, James
; APPLICANT: Goddard, J. Graham
; APPLICANT: Kiefer, Michael
; TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE
; TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR
; FILE REFERENCE: 252/004
; CURRENT APPLICATION NUMBER: US/09/169,205D
; CURRENT FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-225-024-2

Query Match 89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3.3e-130;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGLSEYLNPNKVOEHYNT-KETLETQETTSQROVASAFIVILCCCAIVVENLLVLIAVAR 60
DB 1 MGLSEYLNPNKVOEHYNT-KETLDQETTPKRVASAFIILCCCAIVVENLLVLIAVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLHLEACS 180
DB 121 FSLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLHLEACS 180

QY 181 TVLPLAKHVLCVVTIFSIILLAVVALVRYVVRSSHADMAAPOTLLAKTKVTIVLG 240
DB 181 TVLPLAKHVLCVVTIFSIILLAVVALVRYVVRSSHADVAGQOTLLAKTKVTIVLG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREYL 300
DB 241 VFIIICWLPFAFSLILLDSTCPVRACPVLYKAHYFAFATLNSLLNPVIYTWRSRDLRREYL 300

QY 301 RPLQWRPGVGVGRGGTGPQHLLPLRSSSSSLERGMPTSPTELENTVV 353
DB 301 RPLLCWRQKGATG-RRGNGPGRHLLPLRSSSSSLERGLHMTSPTELENTVV 352

RESULT 14
US-09-262-477-2
Sequence 2, Application US/09262477A
Patent No. 6423508
GENERAL INFORMATION:
APPLICANT: George Livi
APPLICANT: Derek Bergema
APPLICANT: Jeffrey Stadel
APPLICANT: Winnie Chan
APPLICANT: Randall Johnson
APPLICANT: Shelagh Wilson
APPLICANT: Jon Chambers
APPLICANT: Phillippe Robert
APPLICANT: Nassirah Khandoudi
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDE SEQUENCES OF HUMAN EDG-1C AND
METHODS OF SCREENING FOR AGONISTS AND ANTAGONISTS FOR HUMAN
TITLE OF INVENTION: EDG-1C RECEPTOR AND SPHINGOSINE 1-PHOSPHATE LIGAND AND
TITLE OF INVENTION: INTERACTION THEREOF
FILE REFERENCE: GP50006
CURRENT APPLICATION NUMBER: US/09/262,477A
CURRENT FILING DATE: 1999-03-04
EARLIER APPLICATION NUMBER: 60/077,369
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/087,102
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 382
TYPE: PRT
ORGANISM: Human
US-09-262-477-2

Query Match 46.9%; Score 849; DB 2; Length 382;
Best Local Similarity 50.5%; Pred. No. 3.2e-64;

Matches 159; Conservative 60; Mismatches 84; Indels 12; Gaps 2;
QY 3 SLYSEYLNPNKVOEHYNT-KETLETQETTSQROVASAFIVILCCCAIVVENLLVLIAVAR 61
DB 14 SSVSDYVNDYIVRHNTYTKLNISADKENSIKLTSVVFILCCFIIENIFVLLTIWKT 73

QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 121
DB 74 KKFHRPMYVFIIGNLAALSLLAGVAVTANLLSGATTYKLTTPAQWFLREGSMEVALSASF 133

QY 122 SLLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLHLEACST 181
DB 134 SLLATAIERYITMLKKLHNGSNFRLLISACWVLSILGLGLPIMGWNCISALSSCST 193

QY 182 VLPLAKHVLCVVTIFSIILLAVVALVRYVVRSSHADMAAPOTLLA 230
DB 194 VLPLAKHVLCVVTIFSIILLAVVALVRYVVRSSHADMAAPOTLLA 230

QY 231 LKTVTVILGVPIVCMWLPFAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
DB 234 LKTVTVILGVPIVCMWLPFAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290

QY 291 RSRDLRREYLRLPQC 305
DB 314 TNKEMRRAPFIRMSC 328

RESULT 15
US-08-196-989B-4
Sequence 4, Application US/08196989B
Patent No. 5585476
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-196-989B-4

Query Match 46.8%; Score 847; DB 1; Length 383;
Best Local Similarity 48.4%; Pred. No. 4.7e-64;
Matches 167; Conservative 61; Mismatches 103; Indels 14; Gaps 4;

QY 3 SLYSEYLNPNKVOEHYNT-KETLETQETTSQROVASAFIVILCCCAIVVENLLVLIAVAR 61

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Db      15  SQVSDYGNVDIIIVHYNVTGKLNIGVEKDHGIKLTSVWVFILICCLLIILENIFVLLTIWKT 74
Qy      62  SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFPAREGSAPITLSASVF 121
Db      75  KXFHRPMYYFIGNLALSDLLAGVAYTANLLSGATTYKLTPAQWFLREGSMFVALSASVF 134
Qy     122  SLATAIERHVAIAKVLGYGSDKSCRMILLIGASWLLISLVGLPLILGWNCIGHLEACST 181
Db     135  SLATAIERIYITMLKWLHNGNSRSRFLISACWVISLILGGLPIMGWNCISSLSSCST 194
Qy     182  VLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRS-----SHADMAAPQTLA 230
Db     195  VLPLYKHVILFCTVFTLLLSIVILYCRIYSLVTRSRRLTFRKNISKARSSEKSLA 254
Qy     231  LLKTVTVLGVFIVCWLPAFISILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTW 290
Db     255  LLKTVIIVLSVFACWAPLIFILLLDVGCKAKTCDILYKAHYFLVFLAVLNSGTNPDIYTL 314
Qy     291  RSRDLRREVLRLPQCWR-PGVGVQGR-RGGTTPGHLLPLRSSSS 333
Db     315  TNKEMRRAPFIRIISCKCPNGDSAGKFKRPIIPGMFGRSKSDNS 359

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Search completed: December 4, 2005, 06:24:24
 Job time : 34.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:23:26 ; Search time 6 Seconds
(without alignments)
281.714 Million cell updates/sec

Title: US-10-084-507B-22

Perfect score: 1809

Sequence: 1 MGSLSYSEYLNPKVQEHYNY.....LERGMHMTSPTFLEGNTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

- Database : Published Applications AA New:*
- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	481.5	26.6	353	7	US-11-067-884-6
4	284	15.7	360	6	US-10-851-667A-26
5	226.5	12.5	430	6	US-10-992-577-8
6	215.5	11.9	432	6	US-10-992-577-2
7	205.5	11.4	420	6	US-10-992-577-6
8	205.5	11.4	522	6	US-10-510-018-2
9	202.5	11.2	417	6	US-10-992-577-44
10	198	10.9	440	6	US-10-502-893-2
11	184	10.2	342	6	US-10-980-388-118
12	184	10.2	419	7	US-11-067-884-8
13	167.5	9.3	508	6	US-10-980-388-112
14	143	7.9	415	6	US-10-627-633-2
15	143	7.9	485	6	US-10-821-234-934
16	138	7.6	313	7	US-11-095-093-2
17	136	7.5	409	6	US-10-627-633-4
18	126.5	7.0	340	6	US-10-980-388-117
19	126.5	7.0	352	6	US-10-627-633-6
20	125	6.9	287	6	US-10-980-388-66
21	122	6.7	352	7	US-11-068-686-20
22	121	6.7	352	7	US-11-068-686-2
23	118	6.5	355	7	US-11-068-686-4
24	108.5	6.0	350	6	US-10-502-145-1
25	106	5.9	347	6	US-10-131-826A-18

ALIGNMENTS

RESULT 1

US-11-067-884-2
; Sequence 2, Application US/11067884
; Publication No. US20050261252A1

GENERAL INFORMATION:

; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Liliom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-067-884-2

Query Match 28.0%; Score 506; DB 7; Length 364;

Best Local Similarity 34.6%; Pred. No. 4.8e-36;

Matches 117; Conservative 69; Mismatches 122; Indels 30; Gaps 9;

QY	18	NYNKTETQTTTSQVASFIVILCAIVVENLLVIAVARNKSHSAMVLFGLNLA	77
DB	34	NNRSKGHLATEWNTVSKLVMGIGITVCIFIMLANLLVMVAIVNRRFPPIYLMANLAA	93
QY	78	SDLLAGVAVANTLLSGSVTLRLTPQWFARGSGAFITLSASFVLSILAIAIERHVAIAKV	137
DB	94	ADFFAGLAYFYLMFNTGNTNRLTVSTWLLRGLDTSLTASVANLLAIAIERHITVFM	153
QY	138	KLYGDKSCRMILLIGASWLSISLVGLGPIFGWNCILGHLEACSTVLPYAKHYVLCVVTI	197

Db 154 QLHTRMSNRVVVWIIWITWMAIVMGAIPSVGWNCICDIENCSNMAPLYSDSY-LVFWAI 212
Qy 198 FSIILLAV-VALYVRIYCVWR-----SSHADMAAPQ-----TLALLKTVIVLGVFIVC 245
Db 213 FNLVTFVVMVLYAHIFGVVQRTWRMSRHS--SGPRNRQRTMMSLLKTVIVLGAFTIC 270
Qy 246 WLPFAFSILLDVPACPVHSCPIYKAHYLFAVSTLNSLLNPVIYTWRSRLRREVLRLPQC 305
Db 271 WTPGLVLLLDVCCP--QCDVLAYKEFLLAEFNSAMNPIIYSTYRDKEMGATFQILCC 328
Qy 306 WRPGVGQRRRGTPGHLLPLRSSSLER-----GMH 339
Db 329 QR-----SENPTGPRESSD---RSASSLNHTILAGVH 357

RESULT 2

US-11-067-884-4
; Sequence 4, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilioni, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 351
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-067-884-4

Query Match 26.8%; Score 485; DB 7; Length 351;
Best Local Similarity 35.9%; Pred. No. 2.7e-34;
Matches 117; Conservative 57; Mismatches 134; Indels 18; Gaps 4;
Qy 18 YNYKTELETQETTSRQVASAFIVLCCAIIVVENLLIAVARNSKFSAMVFLGNLAA 77
Db 17 YNNSGKELSSHWPRKDVVVALGLTVSVLVLTLLVTAATASNRFRFQPIYLLGNLAA 76
Qy 78 SDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASFSLIAIAIERHVAIAKV 137
Db 77 ADLFAGVAYFLMFHTGPRTLRLSGVFLRQGLDTSLSASVATLLAIAVERHSVMVAV 136
Qy 138 KLYGSDKSCRMILLIGASWLSLVGLPIGWNCILHLEACSTVPLIYAKHYVLCVVTI 197
Db 137 QLHSLRPLGRVVMVLTGVVVAALGGLLPAHSHWCLCALDCRSRMAPLLSRSLAVWALS 196
Qy 198 FSIILLAVVALYVRIYCVVRSASHADMA-----APQTLALLKTVIVLGVFIVCWLP 248
Db 197 SILVFLMVAVTVTRIFVVRVRRVQMAEHSVCHPRYRTTSLVKTIVVILGAFVVCWTP 256
Qy 249 AFSILLD-YACPVHSCPIYKAHYLFAVSTLNSLLNPVIYTWRSRLRREVLRLPQC-- 305
Db 257 GQVLLDGLGC--EESCNVLAKEYFLLEANSILVNAAVYSCRDAEMRRTFRLLCCAC 314

Qy 306 ---WRPGVGQRRRGTPGHLLP 327
Db 315 LRQTSRVHYTSSAQGGASTRIMLP 340
RESULT 3
US-11-067-884-6
; Sequence 6, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilioni, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Virag, Tamas
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-067-884-6

Query Match 26.6%; Score 481.5; DB 7; Length 353;
Best Local Similarity 32.2%; Pred. No. 5.3e-34;
Matches 101; Conservative 73; Mismatches 121; Indels 19; Gaps 5;
Qy 9 LNPKNQVQHYNYKTELETQETTSRQVASAFIVLCCA-----IVVENLLVLAIVARN 62
Db 1 MNECHYDKHMDFFYNSRT-DTVDDMTGTLVILVLCVGTFFCLFFIFFNSLVIAAVIKNR 59
Qy 63 KPHSAMYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASF 122
Db 60 KHPFPFYLLANLANAADFPAIAVFLMFTGVPVSKTLTVNRWFLRQGLDSSLTASLTN 119
Qy 123 LLATAIERHVAIAKVLYGSDKSCRMILLIGASWLSLVGLGGLPIGWNCILHLEACSTV 182
Db 120 LLVIAVERHSIMRVHSNLTKKRVTLILLVWAIAMFGAVPTLGNCLCNISACSSL 179
Qy 183 LPIYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSASHADMAAPQT-----LALL 232
Db 180 APIYSRSLYFVFTVSNLMFAFLIMVVVYIRIYVYVYKRR-TNVLSPHTSGSISRRRTPMKLM 238
Qy 233 KTVTVILGVFTVCWLPAPAFSTILLDYACPVHSCPIYKAHYLFAVSTLNSLLNPVIYTWRS 292
Db 239 KTVMTVLGAFVVCWTPGLVLLLD-GLNCRQCGQVQVHVRWFLALLNSVNPVIYSYKD 297
Qy 293 RDLRREVLRLPQCW 306
Db 298 EDWYGTMKMKICCF 311

RESULT 4

US-10-851-667A-26
; Sequence 26, Application US/10851667A
; Publication No. US20050260608A1
; GENERAL INFORMATION:

```

; APPLICANT: Zimmer, Andreas
; APPLICANT: Karsak, Meliha
; APPLICANT: de Vernejoul, Marie-Christine
; APPLICANT: Bab, Itai
; APPLICANT: Shohami, Esther
; APPLICANT: Mechoulam, Raphael
; TITLE OF INVENTION: METHODS, KITS AND PHARMACEUTICAL COMPOSITIONS FOR DIAGNOSING,
; PREVENTING AND/OR TREATING OSTEOPOROSIS
; FILE REFERENCE: 28030
; CURRENT APPLICATION NUMBER: US/10/851.667A
; CURRENT FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 360
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (63)..(63)
; OTHER INFORMATION: Non-synonymous polymorphism: Gln or Arg
; US-10-851-667A-26

```

Query Match	15.7%;	Score 284;	DB 6;	Length 360;
Best Local Similarity	25.9%;	Pred. No. 2.2e-17;		
Matches	88;	Conservative 65;	Mismatches 133;	Indels 54; Gaps 13;
QY	14	QOEHYNTKETLETOETTSRQVAS----	AFIVILCCAI-----	VVENLLVL-IAVARSKF 64
DB	6	VTRIANGSKDGLSDSNPMKDYMLSGPOKTA	VAVLCTLLGLLSALENAVVLILSSHLR 65	
QY	65	HSAMYLPLGNLAASDLLAGVAF-----	VANTLLSGSVTLRLTPQVFAREGSAFITL 116	
DB	66	RKPSYLFIGSLAGADFLASVVFACSFYNEFH	VGHGVDSKAVFL-----	LKIGSVTMTF 117
QY	117	SASVFSLLAIAIERHVAIAKVLGSKSC----	RMLLIGASWLSILVIGGLPILGNC 172	
DB	118	TASVGSLLLTADRYLCLRPSPSY----	KALLTRGRALVTLGIMVLSALVSYLPLMGWTC 174	
QY	173	LGHLEACSTVLPLYAKHVLCVVTIFSI	LLAVVALVYRI-----	CVVRSSHADMAAP 226
DB	175	CP--RPSCEFLPLNDYLLSWLFLAF	LPFGSGLIYTYGHVLWKAQHVASUSLGHQDRQVP 232	
QY	227	-----QTLALLKTTVTIVLGVFI	VCWLPAPFASILLLDYACPVHSCPILYKAHLYFA--VST 278	
DB	233	GMABMRDLVRKLTGLGLVLA	VLLICWFPVLMAHSLATTLSD----	QVKKAFACSMCLL 289
QY	279	LNLSLLNPVIYTWRSRDLRREVL	RPLQCWRP----	GVGVQGR 315
DB	290	INSMVNPVIYALRGEITSR	SAHHCLAHWKCKVRLGSGEAK 329	

```

RESULT 5
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22

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; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-992-577-8

Query Match      12.5%; Score 226.5; DB 6; Length 430;
Best Local Similarity 24.7%; Pred. No. 1.8e-12;
Matches 102; Conservative 58; Mismatches 120; Indels 133; Gaps 19;

QY      35  VASAFVILCCAIIVENLLVLIVARNRKFSAMYLFLGNLAASDLLAGVAFVANTILSG 94
      Db      48  VAYALIFLLC--MVGNTLVCFVLKRNRMHTVTNNFILNLAVSDLLVGFCFMTPLVDN 104
QY      95  SVTLRLTPQWFAREGSAF-----TTLASVFSLLAIAIER-----HVAIAK 136
      Db     105  LIT-----GWPFDNATCKMSGLVQGSVASVFTLVAlAIVERFCIVHPREK 152
QY     137  VKLYGSDKSCRMILLIGASMLISLVL---GGLPILGNCLGH---LEACSTVLPYAKHYV 191
      Db     153  LTLR-----KALVTAVIWAALLMCPBSAVTLTVTRESHHFNVMDARNSYPLYS---- 202
QY     192  LC-----VVTIPSIIILLAVALYRIYCVVR-----SSHADMAA 225
      Db     203  -CWEAWPEKGMRRVYTVTLFSHIYLAPLIVVMYARIARKLCQAPGAPGGEAADPRA 261
QY     226  PQTALLKTVTVLGVFI-VCNMLPAPSILL--DYA-----CPVHSCPILYKAHYLF 274
      Db     262  SRRARVVMHMLVNAVLFFTLTSLWLPWALLLLIDYGQLSAPQLHLTVYVAFPF---AHWL- 317
QY     275  AVSTLNSLNPVITYTWRSRLRR---EVLRLPQCWRP----- 308
      Db     318  --AFFNSSANPIIYGFENENFRGFQAFARLCPRSGSHKEAYSERPGCLLHRRVFW 375
QY     309  -----GVGVQGRRRGGTGGHLLPLLRSSSSLERGM-----HMP-TSPTF 346
      Db     376  VRPSDGLPSESQSSGAPRPGRLPLRNGVAAHHGLPREGPGCSHLPLTIPAW 428

```

RESULT 6
 US-10-992-577-2
 ; Sequence 2, Application US/10992577
 ; Publication No. US20050260687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerald, Christophe P.G.
 ; APPLICANT: Jones, Kenneth A.
 ; APPLICANT: Bonini, James A.
 ; APPLICANT: Borowsky, Beth E.
 ; APPLICANT: Craig, Douglas A.
 ; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
 ; TITLE OF INVENTION: And Uses thereof
 ; FILE REFERENCE: 57155-D/JPW
 ; CURRENT APPLICATION NUMBER: US/10/992,577
 ; CURRENT FILING DATE: 2004-11-18
 ; PRIOR APPLICATION NUMBER: US/09/538,036
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/405,558
 ; PRIOR FILING DATE: 1999-09-24
 ; PRIOR APPLICATION NUMBER: 09/255,368
 ; PRIOR FILING DATE: 1999-02-22
 ; PRIOR APPLICATION NUMBER: 09/161,113
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-992-577-2

Query Match	11.9%;	Score 215.5;	DB 6;	Length 432;
Best Local Similarity	23.7%;	Pred. No. 1.6e-11;		
Matches 102;	Conservative 57;	Mismatches 140;	Indels 131;	Gaps 19;

QY	21	TKETLEQTETTSROVASAFI---	VILCCAI	VVENLLVLI	AVARSKPHS	AMYLFLGNLAA	77	
Db	28	TSLTFSSYQHSPPVAMFIAAYVLI	FLLCWGVNT	LCFIVL	KRHMRTVT	NMFTLNJAV	87	
QY	78	SDLLAGVAFVANTLLSGSVTLRL	TPVQWFA	REGSAF-----	ITLSASV	FSLL	124	
Db	88	SDLLVGFICMPTTLVDNLIT-----	GWPF	DNATCKMSGL	VQMSVSASV	FTLV	135	
QY	125	AIATER-----	HVAIAK	VLYGSDKSCRM	LLIGASWLISLV---	GGLPILGNWCLGH-	175	
Db	136	AIAYERFCIVHPHREKLTLE---	KALFTIA	VIWALALLIMCPS	AVTLT	VTREHHF	189	
QY	176	-LEACSTVLPYA-----	KHYVLCVVT-	IFSII	LAVVALYVRI-----		212	
Db	190	MLDARNRSYPLYSCWEAWEKGM	RKYTAVL	FAHLYL	VPLALI	VWVYVRIARKLCQAPGP	249	
QY	213	-----	YCVRRSHADMAAPOTL	LALKTTVI	VLGVFI	VCWLP	PAFSILLL-DYA-----	258
Db	250	ARDTEEA	VAEGRTSRRRARVVHML	VMVAL--	FFTLSWL	PLWVLL	LLIDYGE	LSLQLH 306
QY	259	-CPVHSCPILYKAHYLFAVST	LNLSLLNPVI	TWTSRDLRR---	EVL	RP	LCWRRP-----	308
Db	307	LLSVYAFPL--	-AHWL---	AFHSSANPII	YGFNFNFR	FGOAFRAQLC	WPPWAAHKQ 360	
QY	309	-----	GVGQRRRG	GTGPHHLLPL	RRSSSSLSERG--			337
Db	361	AYSERP	NRLRRVVVDVQPS	DSGLP	SESGPSSGV	PGGRULP	LNGRVAHODG	PGGPGC 420
QY	338	MHMP-TSPTF 346						
Db	421	NHMPITPAW 430						

RESULT 7	
US-10-992-577-6	Sequence 6, Application US/10992577
Publication No. US20050260687A1	
GENERAL INFORMATION:	
APPLICANT: Gerald, Christophe P.G.	
APPLICANT: Jones, Kenneth A.	
APPLICANT: Boninl, James A.	
APPLICANT: Borowsky, Beth E.	
APPLICANT: Craig, Douglas A.	
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors	
TITLE OF INVENTION: And Uses Thereof	
FILE REFERENCE: 57155-D/JPW	
CURRENT APPLICATION NUMBER: US/10/992,577	
CURRENT FILING DATE: 2004-11-18	
PRIOR APPLICATION NUMBER: US/09/538,036	
PRIOR FILING DATE: 2000-03-29	
PRIOR APPLICATION NUMBER: 09/405,558	
PRIOR FILING DATE: 1999-09-24	
PRIOR APPLICATION NUMBER: 09/255,368	
PRIOR FILING DATE: 1999-02-22	
PRIOR APPLICATION NUMBER: 09/161,113	
PRIOR FILING DATE: 1998-09-25	
NUMBER OF SEQ ID NOS: 71	
SOFTWARE: PatentIn Ver. 2.1	
SEQ ID NO 6	
LENGTH: 420	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-10-992-577-6	

```

Qy 10 NPNKVOEH-----YNYTKETLETQETTSRQVASAFIVILCAIIVENLLVLIIVARNK 63
Db 18 NVNDTKHLYSDINITYVNYVLIHQPOVAAFIISYFLIFLFC--MMGNVTVCFIVMRNKH 75
Qy 64 FHSAMYLFLGNLAASDLLAGVAFVANTLLS-----GSVTLRLTPVQWFAREGSAPIT 115
Db 76 MHTVTNLFILNLAISDLLVIGFCMPITLLDNIAGPFGNTWCKISGLV---QG---IS 128
Qy 116 LSASFVSLAIAIERHVAIA---KVKLYGSDKSCRMILLIGASWLISLVGLGLPILGWNC 172
Db 129 VAASVFTLVAIADRFQCVVYFEPKPL--TIKTAIVIIMI--IWLAIATI-----174
Qy 173 LGHLEACSTVLPYAKHYV-----LCVTVTFISILLAV 205
Db 175 ---MSPSAVMLHVQEBKYRYRLNSQNTKSPVYWCREDWPQEMRKIYTVTLFANIYLA 231
Qy 206 VALYVRIYCVWRSSHADMAAPOT-----LALLKTVTVILGVFIVCWLPAF 250
Db 232 LSIIVIMYGRIGISLAFRAAVPHTRKNOEQHWHVSRKKQIKMLLIIVALLFISWLPW 291
Qy 251 SILL--DYA-----CPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRLRR 297
Db 292 TLMMLSDYADLSPNELQIINIYIFPAHWL---AFGNSSVNPILYGFNFENFR 342

RESULT 8
US-10-510-018-2
; Sequence 2, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; FILE REFERENCE: Le A 35 945
; CURRENT APPLICATION NUMBER: US/10/510,018
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/002962
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: EP 02007270.8
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-018-2

Query Match 11.4%; Score 205.5; DB 6; Length 522;
Best Local Similarity 23.2%; Pred. No. 1.3e-10;
Matches 82; Conservative 69; Mismatches 108; Indels 95; Gaps 14;

Qy 10 NPNKVOEH-----YNYTKETLETQETTSRQVASAFIVILCAIIVENLLVLIIVARNK 63
Db 120 NVNDTKHLYSDINITYVNYVLIHQPOVAAFIISYFLIFLFC--MMGNVTVCFIVMRNKH 177
Qy 64 FHSAMYLFLGNLAASDLLAGVAFVANTLLS-----GSVTLRLTPVQWFAREGSAPIT 115
Db 178 MHTVTNLFILNLAISDLLVIGFCMPITLLDNIAGPFGNTWCKISGLV---QG---IS 230
Qy 116 LSASFVSLAIAIERHVAIA---KVKLYGSDKSCRMILLIGASWLISLVGLGLPILGWNC 172
Db 231 VAASVFTLVAIADRFQCVVYFEPKPL--TIKTAIVIIMI--IWLAIATI-----276
Qy 173 LGHLEACSTVLPYAKHYV-----LCVTVTFISILLAV 205
Db 277 ---MSPSAVMLHVQEBKYRYRLNSQNTKSPVYWCREDWPQEMRKIYTVTLFANIYLA 333
Qy 206 VALYVRIYCVWRSSHADMAAPOT-----LALLKTVTVILGVFIVCWLPAF 250
Db 334 LSIIVIMYGRIGISLAFRAAVPHTRKNOEQHWHVSRKKQIKMLLIIVALLFISWLPW 393

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QY 251 SILL-DYA-----CPVHSCPILYKAHYLFAVSTLNSLLNPNVIYTWRSRDLRR 297
Db 394 TLMMLSDYADLSPNELQINIYIYFPAHWL---AFGNSSVNIYGFNFENFR 444

RESULT 9
US-10-992-577-44
; Sequence 44, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: And Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPW
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 44
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-44

Query Match 11.2%; Score 202.5; DB 6; Length 417;
Best Local Similarity 22.6%; Pred. No. 1.9e-10;
Matches 89; Conservative 73; Mismatches 117; Indels 115; Gaps 18;

QY 20 YTKETLEQTTSRQVASFIVLCCAIIVENLLVLIIVARNKSHSAMYFLGNLAASD 79
Db 34 YNNYLLHQPHVTAVFSSYFLIFLFC--VGNVTVCFVIRNRYMHTVTFNFIENLAISD 91
QY 80 LLAGAVAVANTLLS-----GSVTIRLTPVQWFAREGSFITLSASVFSLLAIAIERH 131
Db 92 LLVGIFCMPIITLNDNIAGWPFSSMCKISGLV---QG---ISVAASVFTLVAIAVDRF 144
QY 132 VAIA---KVKLYGSDSKRMLLIGASWLISLVGLPIL----- 168
Db 145 RCVVPFPK-----LTVTAFVNIIVGLAITIMTPSAIMLHVQEEKYRVR 193
QY 169 --GWNCLGHLEAGSTVPLYAKHYLVLCVVTIFSIILLAVVALYVRYCVVRSS----- 219
Db 194 LSHNKTSIVYWCREDWPNQEMERIYTV-LFATYIPLSLIVINYARIGASLFTKSAH 252
QY 220 -----HADMAAPQTLALKTVTVLGVFIVCWLPAFSLILL-DYA-----C 259
Db 253 STGKQRLEQHWVSKKQKVIKMLLTVAL--LFLSWLPWLTMLMSDYADLSPNKLRVI 309
QY 260 PVHSCPILYKAHYLFAVSTLNSLLNPNVIYTWRSRDLR-----REVLRPQCWRPG 309
Db 310 NIIVYYPF---AHLW---AFGNSSVNIYIYGFNFENFRSGFDQAFQCKKVPQEQAY--- 360
QY 310 VGVQGRRGGTGPHGLLPLRSSSSSLERGMMHPTS 343
Db 361 -GLRAKRN-----LDINTSGLL---VHEPAS 382
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RESULT 10
US-10-502-893-2
; Sequence 2, Application US/10502893

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; Publication No. US2005025529A1
; GENERAL INFORMATION:
; APPLICANT: Bayer HealthCare AG
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with a New
; TITLE OF INVENTION: Human SHT6 Receptor
; FILE REFERENCE: LeA 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-502-893-2

Query Match 10.9%; Score 198; DB 6; Length 440;
Best Local Similarity 25.0%; Pred. No. 4.7e-10;
Matches 93; Conservative 54; Mismatches 139; Indels 86; Gaps 16;

QY 35 VASAFIVLCCAIIVENLLVLI-----AVARNKSHSAMYFLGNLAASDLLAGVAF--- 86
Db 29 VAAALCVVIALTAANSLLIALICTOPALRNTSNF-----FLVSLFTSDLMVGLVVMPP 82
QY 87 -VANTLLSGSVTLRLTPVQWFAREGSFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS 145
Db 83 AMLNALYGRWVLARGCLLTAFD---VMCCSASILNCLISLDRVLLILSLRYKLRMT 139
QY 146 -CRMILLIGASWLISLVGLGGLP-IILGNCLGHLE-----ACSTVPLPYAKHYLVLCVVTI- 197
Db 140 PURALALVLGAWSLAALASFLPLLLGHWELGHARPPVPGQCRLASL---PFVLVASGLT 196
QY 198 FSIIILLAVVALYVRYCVVRSSHADMA-----APQTLAL----- 231
Db 197 FFLPSGAICFTYCRILLAAKQAVASLTTCMASQASSETLQVPTPRPGVESADSRRLA 256
QY 232 -----LK---TVTVLGVFIVCWLPAFSLILLDYACVPVHSCPILYKAHYLFAVSTLNS 281
Db 257 TKHSRKALKASLTGLIGLGMFFVTWLPFFVANIQAACDCIS-PGLFDV--LTWLGYCNS 313
QY 282 LLNPNVIYTWRSRDLRREVLRPLQCWR-----PGVGVQGRRGGTGPHGLLPLRSSS 332
Db 314 TWPNIYPLFMDFKRALGRFLPCPCPRQASLASPSLRTSHSGPRPG-----L 364
QY 333 SLERGMMHPTSP 344
Db 365 SLQVPLPLPP 376

RESULT 11
US-10-980-388-118
; Sequence 118, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App
; FILE REFERENCE: 00325-US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
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; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-118

Query Match      10.2%; Score 184; DB 6; Length 342;
Best Local Similarity 22.4%; Pred. No. 5,4e-09;
Matches 64; Conservative 53; Mismatches 103; Indels 66; Gaps 11;

Qy 48 VVENLLVLIIVARNKSFHMYFLGNLAASDLLAGVAVANTLGGSVTLRLTPVQWFA 107
Db 46 VFGNLLVMTSVLHFKQLHSPNTNFIASLACADFLGVTVMLFSM-----VRTVESCWF 99

Qy 108 REGSAFITYLS-----ASVFSLLAIAIERHVAIAKVLGSDKSCRM-L-LIGASWL 157
Db 100 --GAKFCTLHSCCDVAFCYSSVHLHCFICIDRIYIVVTDPLVYATKFTVSVSGICISVSMI 157

Qy 158 ISLVGLGLP-----ILGNCLGHLEACSTVLPYAKHYLVLCVWTIFSIIILA 204
Db 158 LPLTSGAVFYTVGNDGLEGELVSALNCVG---GQIIV---SQGWLIDFLFFIPTLV 211

Qy 205 VVALVRYICVVR-----SSHADMAAPQTLALKTTVTIVLGVFIVCWL 247
Db 212 MIILYSKIFLIAKQAKIETTSSKVESSESYKIRVAKRERKAAKTLGVTVLAFLVSWL 271

Qy 248 PAFSILLILD-----YACPVHSCPI-LYKAHYLFAVSTLNSLNPVIY 288
Db 272 PTVVDILIDAPMGFLTPAYIIEICWSAY-----NSAMNPLIY 310
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RESULT 12
US-11-067-884-8
; Sequence 8, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Duane D.
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dalton, James T.
; APPLICANT: Sarder, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
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; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-884-8

Query Match      10.2%; Score 184; DB 7; Length 419;
Best Local Similarity 25.2%; Pred. No. 6.7e-09;
Matches 91; Conservative 50; Mismatches 132; Indels 88; Gaps 17;

Qy 37 SAFIVILCAIVVENLLVLIIVARNKSFHMYFLGNLAASDLLAGV---AFVANTLLS 93
Db 85 SAIMIFILFVSFLGNLVCLMVYQKAMRSAINITLLASLAFADMLLAVLNMPFALVTIL- 143

Qy 94 GSVTLRLTPVQWFAREGSAFITLSA--SVFSLAIAIERHVAIA-----KVLYGSDKSCR 147
Db 144 ---TTRWIFGKFCRVSAWFFWLFVIEGVAILLIISIDRFLIIVQRQDKLPY-----R 194

Qy 148 MLLLIGASWLIS-----LVLGG-----LPIGMNCL-GHLEACSTVLPYAKHYLVLCVWT 196
Db 195 AKVLIIVSWATSPFCVAFPLAVGNPDLQIPSRAPQCVFGY-----TTNPGYQAYVILISLI 249

Qy 197 IFSIILLAVV-----ALYVRIY-----CVRSSHADMAAPQ-----T 228
Db 250 SFFIPFLVILYSFMGIINTLRHNALRIHSYPEGICLSQASKLGLMSLQRPQFQMSIDMGFK 309

Qy 229 LALKTTVTIVLGVFIVCWLPAFSTILLDDYACPVHSCPILYKAHYLFAVST-----INS 281
Db 310 TRAFITLILPAFVIVCWAP-FTTYSLSVATSKH-----FYQHNFPELSTWLLMLCYLKS 364

Qy 282 LLNPVIYTWRSR---DJRREVLRLQCWPRGVGVQRRRGTTGPHHLLPLRSSSSSLERGM 338
Db 365 ALNPLIYVWRIKKFHDACLDNMPKSFPLPQL-----PGHTRKRIRPSAVYVCGE 414

Qy 339 H 339
Db 415 H 415
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RESULT 13
US-10-980-388-112
; Sequence 112, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
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; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-112

Query Match      9.3%; Score 167.5; DB 6; Length 508;
Best Local Similarity 24.7%; Pred. No. 2e-07;
Matches 49; Conservative 48; Mismatches 84; Indels 17; Gaps 6;

QY 35 VASAFIVLCCAVVENLAVLAVARNKPHSAMVFLGNLAASDLLAGVAFVANTLLSG 94
Db 33 IRSTVLVIFLAFASFGVGNVIALVQKPKQLQVTRNFENLAVTDLQ-LSLVAPVAVAT 91

QY 95 SVTLRLTPVQWFAREG--SAFITLS-----ASVFSLAIAIERHVAIAKVLGSKDCSR 147
Db 92 SV-----PLFWPLNSHFCTALVSLTHLPAFASVNTVVVSDRYLSIHPLSPSKMKTOR 146

QY 148 M-LLIGASWLSLVGGPIILGNCLGHLE---ACSTVLPIYAKHYVLCVVTIISIILL 203
Db 147 RGYLLYGTWIVAILQSTPELYGWQAQAFDERNALCSMTWIGASPSVTILSVSVFVIPLEI 206

QY 204 AVVALYVRIYCVVRSSHA 221
Db 207 VMIACSVVFCARROHA 224
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RESULT 14
US-10-627-633-2
; Sequence 2, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brennand, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-633-2

Query Match      7.9%; Score 143; DB 6; Length 415;
Best Local Similarity 24.2%; Pred. No. 1.9e-05;
Matches 86; Conservative 55; Mismatches 128; Indels 86; Gaps 19;
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QY 4 LYSEYL-----NPNKVQEHYNTKLETQETTSROVASAFIVLCCAVVENLILV 54
Db 35 LPSQYLMEISEHWSNQTDLHY-----VLKPEVAT---ASIFFGLMLSPSIFGNSLV 86
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QY 55 LIAVARNSKPHSAMVFLGNLAASDLLAGVAFVANTLLS-----GSVTIURLTPVQWF 106
Db 87 CLVHRSRRTOSTTNYFVVMACADLLISVASTPPVLLQFTTGRWTLGSATCKV--VRVF 144

QY 107 AREGSAFTLSASVPSLLAIAIERHVAIA-----KVKLYGSKDCSCRMILLIGASWLI--S 159
Db 145 -----QYLTGPGVQIYVLLSICIDRFTYTVPLSPKVSREKAKK-----MIAASWIFDAG 193

QY 160 LVLGGLPILGNCLGHLEACSTVLB-----LYAKHYVLCVVTIISIILL-----AVVALY 209
Db 194 FVTPVLFFYGNWDSH---CNYFLPSSWEGTAYTVIHFLVGVPIVPSVLILFYQKVIKYI 250

QY 210 VRIYCVVRSSHADM-AAPQT-LALIKTVITVLGVFIVCWLPAFASILL-----DYACPV 261
Db 251 WRIGTGDRTVTRTWNIVPTKVKTKMFLNLNLLFLLSWLP-FHYAQLWHPHEQDYK--- 306

QY 262 HSCPILYKAHYLFA-----VSTLNSLLNPVITWRSRDLRREV-----LRPLOCWR 307
Db 307 -----KSSLVFTAITWISFSSASKPTLYSIYNANFRGRMKETFCMSSMKCYR 354
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RESULT 15
US-10-821-234-934
; Sequence 934, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PRT_SEQ_genes Version 1.0
; SEQ ID NO 934
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-934
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Query Match      7.9%; Score 143; DB 6; Length 485;
Best Local Similarity 22.7%; Pred. No. 2.2e-05;
Matches 64; Conservative 57; Mismatches 121; Indels 40; Gaps 11;

QY 51 NLLVLIIVARNKPHSAMVFLGNLAASDLL--AGVAFVANTLLSGSVTLRLTPVQW-FA 107
Db 180 NIMAIVFVILKMKVKKPDAVVYMLHLATADLVLPVSVLPFKISYIFSGS-----DWQFG 231

QY 108 REGSAFIT-----LSASVFSLLAIAIERHVAIAKV-----KLYGSKDCSCRMILLIGA 154
Db 232 SELCFVTAAFYCNMYVASILLMTVISIDRFLAVVYPMQSLSWRTLGRASFTCLAIWALAI 291

QY 155 SWLISLVL--GGPLPILGNCLGHLEACSTVL-----PLYAKHYVLCVVTIISIILLAVV 206
Db 292 AGWVPLVLKEQTIQVPGLN-----ITTCHDLNLETLEGYYAYYFSAFVFFVPLIIST 347

QY 207 ALYVRIYCVVRSSHADMAAPQTLALKTVITVLGVFIVCWLPAFASILLDYACPVH--SC 264
Db 348 VCYSIIRCLSSAVANRKKSRALFLSAA-VFCFIICFGTNPVLLIAHYFSLSHSTYT 406

QY 265 PLYKAHYL-FAVSTLNSLLNPVITWRSRDLRREVLRPLOC 305
Db 407 EAAFYALLCVCVSSISSCIDPLIYYASSECQRYVYSILCC 448
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Job time : 7 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:23:06 ; Search time 115.5 Seconds
(without alignments)
1277.002 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLYSEYLNPNKVOEHYNY.....LERGMHPTPTFLRGNTVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:*
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1809	100.0	353	3	US-09-731-030A-19 Sequence 19, Appl
2	1809	100.0	353	4	US-10-084-507B-22 Sequence 22, Appl
3	1804	99.7	353	3	US-09-771-063-2 Sequence 2, Appl
4	1803	99.7	353	4	US-10-084-507B-17 Sequence 17, Appl
5	1787	98.8	353	3	US-09-842-316-8 Sequence 8, Appl
6	1787	98.8	353	3	US-09-971-228-9 Sequence 9, Appl
7	1787	98.8	353	3	US-09-904-099-33 Sequence 33, Appl
8	1787	98.8	353	4	US-10-225-567A-508 Sequence 508, App
9	1787	98.8	353	4	US-10-228-762-19 Sequence 19, Appl
10	1787	98.8	353	4	US-10-393-870-3 Sequence 3, Appl
11	1787	98.8	353	4	US-10-421-828-8 Sequence 8, Appl
12	1787	98.8	353	4	US-10-715-117-7 Sequence 7, Appl
13	1787	98.8	353	5	US-10-498-848-46 Sequence 46, Appl
14	1783	98.6	353	3	US-09-771-063-4 Sequence 4, Appl
15	1625.5	89.9	352	4	US-10-084-507B-21 Sequence 21, Appl
16	1432	79.2	372	3	US-09-904-099-37 Sequence 37, Appl
17	946	52.3	269	3	US-09-764-886-47 Sequence 47, Appl
18	946	52.3	269	3	US-09-764-886-47 Sequence 47, Appl
19	946	52.3	274	3	US-09-764-886-74 Sequence 74, Appl
20	946	52.3	274	3	US-09-764-891-5338 Sequence 5338, Ap
21	946	52.3	274	3	US-09-764-886-74 Sequence 74, Appl
22	860.5	47.6	384	3	US-09-904-099-5 Sequence 5, Appl
23	858.5	47.5	384	3	US-09-904-099-4 Sequence 4, Appl
24	858	47.4	391	3	US-09-904-099-3 Sequence 3, Appl
25	854.5	47.2	362	3	US-09-993-844-8 Sequence 8, Appl
26	854.5	47.2	362	4	US-10-633-438-65 Sequence 65, Appl
27	854.5	47.2	362	5	US-10-901-772-65 Sequence 65, Appl

28	854.5	47.2	362	6	US-11-026-435-8	Sequence 8, Appl
29	849	46.9	341	3	US-09-971-228-13	Sequence 13, Appl
30	849	46.9	382	3	US-09-971-228-5	Sequence 5, Appl
31	849	46.9	382	3	US-09-863-455-2	Sequence 2, Appl
32	849	46.9	382	3	US-09-759-514-2	Sequence 2, Appl
33	849	46.9	382	3	US-09-904-099-1	Sequence 1, Appl
34	849	46.9	382	4	US-10-087-192-786	Sequence 786, App
35	849	46.9	382	4	US-10-225-567A-237	Sequence 237, App
36	849	46.9	382	4	US-10-295-027-2	Sequence 2, Appl
37	849	46.9	382	4	US-10-429-160-72	Sequence 72, Appl
38	849	46.9	382	4	US-10-211-462-2	Sequence 2, Appl
39	849	46.9	382	5	US-10-491-545A-30	Sequence 30, Appl
40	849	46.9	382	5	US-10-498-848-38	Sequence 38, Appl
41	849	46.9	448	4	US-10-425-114-55760	Sequence 55760, A
42	848	46.9	346	3	US-09-971-228-15	Sequence 15, Appl
43	847	46.8	383	6	US-11-100-593-8	Sequence 8, Appl
44	845	46.7	382	3	US-09-969-711-2	Sequence 2, Appl
45	845	46.7	382	4	US-10-087-192-783	Sequence 783, App

ALIGNMENTS

RESULT 1

US-09-731-030A-19
; Sequence 19, Application US/09731030A
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G
; APPLICANT: GUPTA, Ashwani K.
; TITLE OF INVENTION: ZASTAWNY, Roman L.
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731, 030A
; PRIOR FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

Query Match	100.0%;	Score 1809;	DB 3;	Length 353;
Best Local Similarity	100.0%;	Pred. No. 3.4e-156;		
Matches 353;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGSLYSEYLNPNKVOEHYNYTKETLETTQTTSRQVASAFIVILCCAIIVVENLLVLAVAR	60	
Db	1	MGSLYSEYLNPNKVOEHYNYTKETLETTQTTSRQVASAFIVILCCAIIVVENLLVLAVAR	60	
QY	61	NSKFSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPQWFARGSAFITLSASV	120	
Db	61	NSKFSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPQWFARGSAFITLSASV	120	
QY	121	FSLLAIAIERHVAIAKVKLYGSKCRMLLLIGASWLSLVLGGLPILGWNCLHLEACS	180	
Db	121	FSLLAIAIERHVAIAKVKLYGSKCRMLLLIGASWLSLVLGGLPILGWNCLHLEACS	180	
QY	181	TVLPYAKHYVLCVWTIFSIILLAVVALVYRIVCYVRRSHADMAAPQTALLKTVIVLG	240	
Db	181	TVLPYAKHYVLCVWTIFSIILLAVVALVYRIVCYVRRSHADMAAPQTALLKTVIVLG	240	
QY	241	VFIVCWLPFAFSTILLDYACPVHSCPTLYKAHYLFAVSTLNSLLNPVITYWRSRDLRREV	300	
Db	241	VFIVCWLPFAFSTILLDYACPVHSCPTLYKAHYLFAVSTLNSLLNPVITYWRSRDLRREV	300	
QY	301	RPLQCRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMPPTSPTFLEGNTVV	353	

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Db 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLRGMHMTSPTFLEGNVTW 353

RESULT 2
US-10-084-507B-22
; Sequence 22, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084,507B
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-507B-22

Query Match 100.0%; Score 1809; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 3.4e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKQVEHYNYTKETLETTTSRQVASAFIVILCCAIIVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKQVEHYNYTKETLETTTSRQVASAFIVILCCAIIVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFILTASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFILTASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKKTIVILG 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKKTIVILG 240
QY 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYVWRSRDLRREV 300
Db 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYVWRSRDLRREV 300
QY 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLRGMHMTSPTFLEGNVTW 353
Db 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLRGMHMTSPTFLEGNVTW 353

RESULT 3
US-09-771-063-2
; Sequence 2, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derk J. Bergsma
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
```

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; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-C1
; CURRENT APPLICATION NUMBER: US/09/771,063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-771-063-2

Query Match 99.7%; Score 1804; DB 3; Length 353;
Best Local Similarity 99.4%; Pred. No. 9.7e-156;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKQVEHYNYTKETLETTTSRQVASAFIVILCCAIIVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKQVEHYNYTKETLETTTSRQVASAFIVILCCAIIVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFILTASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFILTASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKKTIVILG 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKKTIVILG 240
QY 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYVWRSRDLRREV 300
Db 241 VFIVCWLPAPFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYVWRSRDLRREV 300
QY 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLRGMHMTSPTFLEGNVTW 353
Db 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLRGMHMTSPTFLEGNVTW 353

RESULT 4
US-10-084-507B-17
; Sequence 17, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084,507B
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 353
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: (273)
OTHER INFORMATION: Leu or Phe
US-10-084-507B-17

Query Match 99.7%; Score 1803; DB 4; Length 353;
Best Local Similarity 99.4%; Pred. No. 1.2e-155; Mismatches 1; Indels 0; Gaps 0;
Matches 351; Conservative

QY 1 MGSLSYSEYLNPNKQVQHYNTKETLETTQTSRQVASFIVILCCAIVVENLLVLIASV 60
DB 1 MGSLSYSEYLNPNKQVQHYNTKETLETTQTSRQVASFIVILCCAIVVENLLVLIASV 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
QY 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353
DB 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353

RESULT 5
US-09-842-316-8
Sequence 8, Application US/09842316
Patent No. US20020099191A1
GENERAL INFORMATION:
APPLICANT: GASSENHUBER, Johann
TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
FILE REFERENCE: 38005-147
CURRENT APPLICATION NUMBER: US/09/842,316
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: EP 116589.3
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: EP 108858.2
PRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
US-09-842-316-8

Query Match 98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154; Mismatches 3; Indels 0; Gaps 0;
Matches 349; Conservative

QY 1 MGSLSYSEYLNPNKQVQHYNTKETLETTQTSRQVASFIVILCCAIVVENLLVLIASV 60
DB 1 MGSLSYSEYLNPNKQVQHYNTKETLETTQTSRQVASFIVILCCAIVVENLLVLIASV 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
QY 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353
DB 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353

DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
QY 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353
DB 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353

RESULT 6
US-09-971-228-9
Sequence 9, Application US/09971228
Patent No. US20020155512A1
GENERAL INFORMATION:
APPLICANT: Liao, X. Charlene
APPLICANT: Chu, Peter
APPLICANT: Pardo, Jorge
APPLICANT: Li, Congfen
APPLICANT: Zhao, Haoran
APPLICANT: Jiang, Yingping
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration
FILE REFERENCE: 021044-000310US
CURRENT APPLICATION NUMBER: US/09/971,228
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/284,763
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 353
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human endothelial differentiation G-protein
OTHER INFORMATION: coupled receptor (GPCR) 5 (EDG5)
US-09-971-228-9

Query Match 98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154; Mismatches 3; Indels 0; Gaps 0;
Matches 349; Conservative

QY 1 MGSLSYSEYLNPNKQVQHYNTKETLETTQTSRQVASFIVILCCAIVVENLLVLIASV 60
DB 1 MGSLSYSEYLNPNKQVQHYNTKETLETTQTSRQVASFIVILCCAIVVENLLVLIASV 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGGPLILGWNCLIGHLEACS 180
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVALYVRIYCVVRSRSHADMAAPQTALLKTKVTIVLG 240
QY 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353
DB 301 RPLQWRPGVGQGRRRGTGPHHLLPLRSSSSSLRGMHMTPTPTFLEGNVTV 353

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RESULT 7
US-09-904-099-33
; Sequence 33, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Shankar, Geetha
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-099-33

Query Match      98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MGSLSYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIYVENLLVLIAR 60
Db      1 MGSLSYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIYVENLLVLIAR 60

Qy      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy      121 FSLAIAIERHVAIAKVLYGSDKSCRMLLIIGASWLSISLVGLPILGNWCLGHEACS 180
Db      121 FSLAIAIERHVAIAKVLYGSDKSCRMLLIIGASWLSISLVGLPILGNWCLGHEACS 180

Qy      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYRIYCVVRSSHADMAAPQTLALLKTVTVILG 240
Db      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYRIYCVVRSSHADMAAPQTLALLKTVTVILG 240

Qy      241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db      241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy      301 RPLQCMRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNITVV 353
Db      301 RPLQCMRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNITVV 353

RESULT 8
US-10-225-567A-508
; Sequence 508, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Rough, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 508
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-508

Query Match      98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MGSLSYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIYVENLLVLIAR 60
Db      1 MGSLSYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIYVENLLVLIAR 60

Qy      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy      121 FSLAIAIERHVAIAKVLYGSDKSCRMLLIIGASWLSISLVGLPILGNWCLGHEACS 180
Db      121 FSLAIAIERHVAIAKVLYGSDKSCRMLLIIGASWLSISLVGLPILGNWCLGHEACS 180

Qy      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYRIYCVVRSSHADMAAPQTLALLKTVTVILG 240
Db      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYRIYCVVRSSHADMAAPQTLALLKTVTVILG 240

Qy      241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db      241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy      301 RPLQCMRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNITVV 353
Db      301 RPLQCMRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNITVV 353

RESULT 9
US-10-228-762-19
; Sequence 19, Application US/10228762
; Publication No. US20030130493A1
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Huang, Ling Yan
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Salton, John A.
; APPLICANT: Wilson, Amy
; APPLICANT: Nagorny, Raisa
; TITLE OF INVENTION: DNA Encoding Edg7 Receptor
; FILE REFERENCE: 58230-a
; CURRENT APPLICATION NUMBER: US/10/228,762
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US/09/356,315
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 09/253,998
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in ver. 2.0 - beta
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-228-762-19

Query Match      98.8%; Score 1787; DB 4; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 MGSLSYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIYVENLLVLIAR 60
Db      1 MGSLSYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIYVENLLVLIAR 60

Qy      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db      61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120

Qy      121 FSLAIAIERHVAIAKVLYGSDKSCRMLLIIGASWLSISLVGLPILGNWCLGHEACS 180
Db      121 FSLAIAIERHVAIAKVLYGSDKSCRMLLIIGASWLSISLVGLPILGNWCLGHEACS 180

Qy      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYRIYCVVRSSHADMAAPQTLALLKTVTVILG 240
Db      181 TVLPLYAKHYVLCVVTIFSIILLAVVALYRIYCVVRSSHADMAAPQTLALLKTVTVILG 240

Qy      241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db      241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300

Qy      301 RPLQCMRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNITVV 353
Db      301 RPLQCMRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNITVV 353
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QY 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVILG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVV 353
Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVV 353

RESULT 10

US-10-393-870-3
; Sequence 3, Application US/10393870
; Publication No. US20030219808A1
; GENERAL INFORMATION:
; APPLICANT: KOZIAN, Detlef
; APPLICANT: KOSTENIS, Evi
; APPLICANT: SIELGER, Karl-Ernet
; APPLICANT: JACOBS, Martina
; APPLICANT: RICARD, Sylvain
; APPLICANT: MACE, Sandrine
; APPLICANT: DELEUZE, Jean-Francois
; TITLE OF INVENTION: ASSOCIATION OF EDG5 POLYMORPHISM WITH TYPE II DIABETES MELLITUS,
; FILE REFERENCE: DEAV2002/0019 US NP
; CURRENT APPLICATION NUMBER: 2003-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-870-3

Query Match 98.8%; Score 1787; DB 4; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLGLEACS 180
QY 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVILG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVV 353
Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVV 353

RESULT 11

US-10-421-828-8
; Sequence 8, Application US/10421828
; Publication No. US20030219874A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIS, Eva

; APPLICANT: GASENHUBER, Johann
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/10/421,828
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-421-828-8

Query Match 98.8%; Score 1787; DB 4; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASAFIVILCCAIVVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSILVGLGPIILGNCLGLEACS 180
QY 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVILG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLLAKTTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVV 353
Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVV 353

RESULT 12

US-10-715-117-7
; Sequence 7, Application US/10715117
; Publication No. US20040171037A1
; GENERAL INFORMATION:
; APPLICANT: LI, JING
; APPLICANT: POWERS, SCOTT
; APPLICANT: SIN, WUN CHEY
; APPLICANT: YANG, JIANXIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
; FILE REFERENCE: 38002-0062
; CURRENT APPLICATION NUMBER: US/10/715,117
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: 60/427,202
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/434,434
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-117-7

Query Match 98.8%; Score 1787; DB 4; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;

Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MGSLYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPILGNWCLGHEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPILGNWCLGHEACS 180
Qy 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Qy 241 VFIVCWLPAFASILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db 241 VFIVCWLPAFASILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Qy 301 RPLOCWRPGVGQRRRGCTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLOCWRPGVGQRRRGCTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 13
US-10-498-848-46
; Sequence 46, Application US/10498848
; Publication No. US20050153289A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Method of Analyzing Gene Expression
; FILE REFERENCE: P02-0155PCT
; CURRENT APPLICATION NUMBER: US/10/498,848
; PRIOR FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: JP 2001-382053
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: JP 2002-45104
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: JP 2002-140111
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: JP 2002-333769
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 46
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human
US-10-498-848-46

Query Match 98.8%; Score 1787; DB 5; Length 353;
Best Local Similarity 98.9%; Pred. No. 3.4e-154;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MGSLYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPILGNWCLGHEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPILGNWCLGHEACS 180
Qy 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Qy 241 VFIVCWLPAFASILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300

Db 241 VFIVCWLPAFASILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Qy 301 RPLOCWRPGVGQRRRGCTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLOCWRPGVGQRRRGCTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353
RESULT 14
US-09-771-063-4
; Sequence 4, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derk J. Bergema
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-C1
; CURRENT APPLICATION NUMBER: US/09/771.063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-771-063-4

Query Match 98.6%; Score 1783; DB 3; Length 353;
Best Local Similarity 98.6%; Pred. No. 8e-154;
Matches 348; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MGSLYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
Db 1 MGSLYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPILGNWCLGHEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPILGNWCLGHEACS 180
Qy 181 TVPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
Qy 241 VFIVCWLPAFASILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db 241 VFIVCWLPAFASILLLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREV 300
Qy 301 RPLOCWRPGVGQRRRGCTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLOCWRPGVGQRRRGCTPGHLLPLRSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 15
US-10-084-507B-21
; Sequence 21, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH

APPLICANT: VYAS, TEJAL B.
APPLICANT: GUPTA, ASHWANI K.
TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
FILE REFERENCE: 108074-00023
CURRENT APPLICATION NUMBER: US/10/084,507B
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/222,995
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/080,610
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/070,185
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 352
TYPE: PRT
ORGANISM: Rattus sp.
US-10-084-507B-21

Query Match 89.9%; Score 1625.5; DB 4; Length 352;
Best Local Similarity 89.5%; Pred. No. 1.8e-139;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY	1	MGSLYSEYLNPNKVOEHYNTKETLETTSTROVASAFIVILCCCAIVVENLLVLI	60
DB	1	MGGLYSEYLNPEKVOEHYNTKETLDMQETPSRKVASAFIILCCCAIVVENLLVLI	60
QY	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAFITLS	120
DB	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSAFITLS	120
QY	121	FSLLAIAIERHVAIAKVLGYSDKSCRMILLIGASWLSISLVGLGPLGWNCLGHLE	180
DB	121	FSLLAIAIERQVAIAKVLGYSDKSCRMMLIGASWLSISLVGLGPLGWNCLDHLE	180
QY	181	TVLPLYAKHYVLCVWTIFSIILLAVVALYVRYCVVRS SHADMAAPQTLALKTV	240
DB	181	TVLPLYAKHYVLCVWTIFSVILLAI VALYVRYFVVRSSHADVAGPQTLLALKTV	240
QY	241	VFTVCWLPAPFISILLDYACPVHSCPTLYKAHYLFAVSTLNSLNPVIYTWRSRDL	300
DB	241	VFTICWLPAPFISILLDDSTCPVRACPVLYKAHYFFAFATLNSLNPVIYTWRSRDL	300
QY	301	RPLQCWRPGVGQRRGGTGGHLLPLRSSSSLERGMHMTSPTFLEGNTVV	353
DB	301	RPLLCWRQKGATG-RRGGNPGHRLPLRSSSSLERGLHMTSPTFLEGNTVV	352

Search completed: December 4, 2005, 06:42:09
Job time : 116.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2005, 06:38:02 ; Search time 152 seconds
(without alignments)
1638.497 Million cell updates/sec

Title: US-10-084-507B-22

Perfect score: 1809

Sequence: 1 MGSLYSEVLNPNKQVHYNY.....LERGMHMTPTPTFLEGNVTW 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1804	99.7	353	1 EDG5 HUMAN	Q95136 homo sapien
2	1631.5	90.2	352	2 Q8C3Q7_MOUSE	Q8C3Q7 m mus muscu
3	1625.5	89.9	352	1 EDG5 RAT	P47752 rattus norv
4	1625.5	89.9	352	2 Q5A1I6 RAT	Q5A1I6 rattus norv
5	1622.5	89.7	352	1 EDG5 MOUSE	P52592 mus musculus
6	998	55.2	370	1 EDG5 BRARE	Q918K8 brachydanio
7	932	51.5	202	2 Q91XR0_CAVPO	Q91XR0 cavia porce
8	869	48.0	190	2 Q9ESK0_RAT	Q9ESK0 rattus norv
9	856	47.3	382	2 Q5R7A1_PONPY	Q5R7A1 pongo pygma
10	849	46.9	382	2 Q9NYN8_HUMAN	Q9NYN8 homo sapien
11	847	46.8	383	1 EDG1 RAT	P48303 rattus norv
12	847	46.8	383	2 Q4V7F6 RAT	Q4V7F6 rattus norv
13	845	46.7	382	2 Q9DC35_MOUSE	Q9DC35 m mus muscu
14	844	46.7	382	2 Q5B1P0_BOVIN	Q5B1P0 bos taurus
15	841	46.5	373	2 Q4T9E2_TETNG	Q4T9E2 tetraodon n
16	839	46.4	382	1 EDG1 MOUSE	Q08530 mus musculus
17	837	46.3	375	2 Q5U389_BRARE	Q5U389 brachydanio
18	837	46.3	382	2 Q5E9P3_BOVIN	Q5E9P3 bos taurus
19	836.5	46.2	381	1 EDG1 HUMAN	P21453 homo sapien
20	835	46.2	374	2 Q6GLU6_XENLA	Q6GLU6 xenopus lae
21	822.5	45.5	326	2 Q99NR8_CASCN	Q99NR8 castor cana
22	820.5	45.4	325	2 Q71BN5_OTOGA	Q71BN5 otolemur ga
23	819	45.3	325	2 Q9BF55_ARTJA	Q9BF55 artibeus ja
24	817	45.2	362	1 EDG1 BRARE	Q9ddk4 brachydanio
25	816.5	45.1	326	2 Q6JC76_9EUTH	Q6JC76 solenodon p
26	816.5	45.1	326	2 Q9BF73_CONCR	Q9BF73 condylura c
27	816.5	45.1	326	2 Q99NR0_9HYST	Q99NR0 cavia tscu
28	816.5	45.1	326	2 Q99NR4_HYSTR	Q99NR4 hystrix bra
29	816	45.1	326	2 Q8MK87_TADBR	Q8MK87 tadaria br
30	815.5	45.1	326	2 Q99NQ7_AGOTA	Q99NQ7 agouti tacz
31	814	45.0	326	2 Q99NR1_HETGA	Q99NR1 heteroceph

RESULT 1
EDG5_HUMAN
ID EDG5_HUMAN STANDARD; PRT; 353 AA.
AC Q95136; Q86UN8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
DE (Endothelial differentiation G-protein coupled receptor 5)
DE (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Name=EDG5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX PubMed=10617617; DOI=10.1074/jbc.275.1.288;
RA An S., Zheng Y., Bleu T.;
RT "Sphingosine 1-phosphate-induced cell proliferation, survival, and related signaling events mediated by G protein-coupled receptors Edg3 and Edg5.";
RT J. Biol. Chem. 275:288-296(2000).
RL [2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.J., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

32 813.5 45.0 326 2 Q9BF72_SORAR Q9BF72 sorex arane
33 813.5 45.0 326 2 Q99NQ9_HYDHO Q99NQ9 hydrochoeru
34 812.5 44.9 326 2 Q9BF75_MYRTR Q9BF75 myrmecophag
35 812.5 44.9 326 2 Q9BF76_TAMTE Q9BF76 tamandua te
36 812.5 44.9 326 2 Q99NR3_EREDO Q99NR3 erethizon d
37 811.5 44.9 326 2 Q9BF74_ERICO Q9BF74 erinaceus c
38 811.5 44.9 326 2 Q9BF79_CHOHO Q9BF79 choleopus h
39 811.5 44.9 326 2 Q99NR5_MOUSE Q99NR5 mus musculu
40 811 44.8 292 2 Q91XR2_CAVPO Q91XR2 cavia porce
41 809.5 44.7 325 2 Q99NR9_TAMST Q99NR9 tamias stri
42 807.5 44.6 326 2 Q8MK86_MEGLY Q8MK86 megaderma l
43 807.5 44.6 326 2 Q9BF66_ELERU Q9BF66 elephantulu
44 806.5 44.6 326 2 Q9BF65_ORYAF Q9BF65 orycteropus
45 805.5 44.5 325 2 Q9BF41_PANON Q9BF41 panthera on

ALIGNMENTS

CC -|- FUNCTION: Receptor for the lysophospholipid sphingosine 1-phosphate (S1P). S1P is a bioactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues. When expressed in rat HTC4 hepatoma cells, is capable of mediating S1P-induced cell proliferation and suppression of apoptosis.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----

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DR EMBL; AF034780; AAC98919.1; -; mRNA.

DR EMBL; AY262688; AAP20652.1; -; Genomic_DNA.

DR EMBL; BC069598; AAH69598.1; -; mRNA.

DR Ensembl; ENSG00000175898; Homo sapiens.

DR HGNC; HGNC:3169; EDG5.

DR MIM; 605111; -.

DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.

DR GO; GO:0008289; F:lipid binding; TAS.

DR GO; GO:0008289; P:activation of MAPK; TAS.

DR GO; GO:0000187; P:protein coupled receptor protein signalin. .; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.

DR InterPro; IPR004063; EDG5_receptor.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR InterPro; IPR004061; S1P_receptor.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR01525; EDG5RECEPTOR.

DR PRINTS; PR00237; GPCRHOOPS.

DR PRINTS; PR01523; S1PRECEPTOR.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Glycoprotein; Lipoprotein;

KW Multigene family; Palmitate; Receptor; Transducer; Transmembrane.

FT TOPO_DOM 1 34 Extracellular (Potential).

FT TRANSMEM 35 59 1 (Potential).

FT TOPO_DOM 60 66 Cytoplasmic (Potential).

FT TRANSMEM 67 95 2 (Potential).

FT TOPO_DOM 96 109 Extracellular (Potential).

FT TRANSMEM 110 128 3 (Potential).

FT TOPO_DOM 129 147 Cytoplasmic (Potential).

FT TRANSMEM 148 173 4 (Potential).

FT TOPO_DOM 174 189 Extracellular (Potential).

FT TRANSMEM 190 210 5 (Potential).

FT TOPO_DOM 211 233 Cytoplasmic (Potential).

FT TRANSMEM 234 255 6 (Potential).

FT TOPO_DOM 256 271 Extracellular (Potential).

FT TRANSMEM 272 292 7 (Potential).

FT TOPO_DOM 293 353 Cytoplasmic (Potential).

FT LIPID S-palmitoyl cysteine (By similarity).

FT CARBOHYD 19 19 N-linked (GlcNAc. .) (Potential).

FT CONFLICT 113 113 F -> S (in Ref. 1).

FT CONFLICT 318 318 G -> V (in Ref. 1).

SQ SEQUENCE 353 AA; 38867 MW; 8E37084284AB7E8 CRC64;

Query Match 99.7%; Score 1804; DB 1; Length 353;

Best Local Similarity 99.4%; Pred. No. 4.7e-114;

Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKQVHNYTKETLETQETTSRQVASAFIVILCAIVENLLVLIASV 60

Db 1 MGSLSYELNPNKQVHNYTKETLETQETTSRQVASAFIVILCAIVENLLVLIASV 60

QY 61 NSKFHSMYLFIGNAASDLGAVFVANTLLSGSVTLRLTPVQVAREGSAFILTASV 120

Db 61 NSKFHSMYLFIGNAASDLGAVFVANTLLSGSVTLRLTPVQVAREGSAFILTASV 120

QY 121 FSLLAIAIERHVAIAKVLKSGDKSCRMILLITGASWLSLVLGGLPILGWNCLGLEACS 180

Db 121 FSLLAIAIERHVAIAKVLKSGDKSCRMILLITGASWLSLVLGGLPILGWNCLGLEACS 180

QY 181 TVPLPYAKHYVLCVVTTFISILLAVVALYVRIYCVVSSHADMAAPOTLALKTKVTIVLG 240

Db 181 TVPLPYAKHYVLCVVTTFISILLAVVALYVRIYCVVSSHADMAAPOTLALKTKVTIVLG 240

QY 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Db 241 VFIVCWLPAFISILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQRRRGSTPGHHLLPLRSSSSSLERGMHMTPTSTFLEGNTVW 353

Db 301 RPLQWRPGVGVQRRRGSTPGHHLLPLRSSSSSLERGMHMTPTSTFLEGNTVW 353

RESULT 2

Q8C3Q7_MOUSE

ID Q8C3Q7_MOUSE PRELIMINARY; PRT; 352 AA.

AC Q8C3Q7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430039A03 product:endothelial differentiation, sphingolipid G-protein-coupled receptor, 5, full insert sequence (Endothelial differentiation, sphingolipid G-protein-coupled receptor, 5).

DE Name=Edg5;

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Marzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RA The FANTOM Consortium,

RT the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE

RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RN Genome Res. 10:1617-1630(2000).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama K., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22389257; PubMed=12479752; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AC085114; BAC39368.1; -; mRNA.
DR EMBL; BC098760; AH98760.1; -; mRNA.
DR Ensembl; ENSMUSG0000043895; Mus musculus.
DR MGI; MGI:99569; Edg5.
DR GO; GO:0007610; P:behavior; IMP.
DR InterPro; IPR004063; EDG5 receptor.
DR InterPro; IPR000276; GPCR Rhodop.
DR InterPro; IPR004061; SLP_Receptor.

DR Pfam; PF00001; 7cm 1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
KW PROSITE; PS02662; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 38829 MW; 6A3E426B0FE54406 CRC64;
Query Match 90.2%; Score 1631.5; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 2.1e-102; Indels 1; Gaps 1;
Matches 318; Conservative 13; Mismatches 21;
QY 1 MGSLYSEYNPNKQEHYNYTKETLETTTSQVASFIVILCCAIIVENLLVLIIVAR 60
DB 1 MGGLYSEYNPEKVLHNYTKETLDMQETTSRKVASAFIILCCAIIVENLLVLIIVAR 60
QY 61 NSKFSHSMYFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFILTASV 120
DB 61 NSKFSHSMYFLGNLAASDLLAGVAVANTLLSGHVTLSLTPVQVFAREGSAFILTASV 120
QY 121 FSLAIAIERHVAIAKVLGSDKSCRMLLIGASWLSLVGLGPIILGMNCLGHLEACS 180
DB 121 FSLAIAIERQVALAKVKLYGSDKSCRMMLIGASWLSLVGLGPIILGMNCLGHLEACS 180
QY 181 TVLPYAKHYVLCVVTFISIIILLAVVALYVRIYCVRRSHADMAAPOTLALLKTVTVILG 240
DB 181 TVLPYAKHYVLCVVTFISVILLAIVALYVRIYFVRRSHADVAGPQTALLKTVTVILG 240
QY 241 VFIICWLPAPFSLILLDYACPVHSCPIILYKHYLPAVSTLNSLLNPVIYTWRSRDURREV 300
DB 241 VFIICWLPAPFSLILLDYACPVHSCPIILYKHYLPAVSTLNSLLNPVIYTWRSRDURREV 300
QY 301 RPLQCRPGVGVQGRRGCTPGHLLPLRSSSLERGMHMTPTPTFLSGNTVV 353
DB 301 RPLQCRPGVGVQGRRGCTPGHLLPLRSSSLERGMHMTPTPTFLSGNTVV 352
RESULT 3
EDG5_RAT
ID EDG5_RAT STANDARD; PRT; 352 AA.
AC P47752;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5) (G-protein
DE coupled receptor H218) (AGRI6) (Endothelial differentiation G-protein
DE coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Name=Edg5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain and Lung;
RX MEDLINE=94373324; PubMed=8087418; DOI=10.1006/mcne.1994.1024;
RA MacLennan A.J., Browe C.S., Gaskin A.A., Lado D.C., Shaw G.;
RT "Cloning and characterization of a putative G-protein coupled receptor
RT potentially involved in development.";
RL Mol. Cell. Neurosci. 5:201-209(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aortic smooth muscle;
RX MEDLINE=93176155; PubMed=8382486;
RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
RA Takawa Y.;
RT "Molecular cloning of a novel putative G protein-coupled receptor
RT expressed in the cardiovascular system.";
RL Biochem. Biophys. Res. Commun. 190:1104-1109(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;

RX MEDLINE=98072391; PubMed=9409733; DOI=10.1016/S0014-5793(97)01301-X;
RA An S., Bleu T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl E.J.;
RT "Identification of cDNAs encoding two G protein-coupled receptors for
RL lysophospholipids.";
RN FEBS Lett. 417:279-282 (1997).
[4]
RP PHARMACOLOGICAL CHARACTERIZATION.
RX PubMed=10393399; DOI=10.1074/jbc.274.27.18997;
RA Ancellin N., Hia T.;
RT "Differential pharmacological properties and signal transduction of
the sphingosine 1-phosphate receptors EDG-1, EDG-3, and EDG-5.";
RL J. Biol. Chem. 274:18997-19002(1999).
CC -!- FUNCTION: Receptor for the lysophospholipid sphingosine 1-
phosphate (S1P). S1P is a bioactive lysophospholipid that elicits
CC diverse physiological effect on most types of cells and tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in all developing tissues with
CC highest levels detected in primitive, transformed cells. Relative
CC abundance; lung > kidney = skin = gut > spleen > brain > liver.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U10699; AA19241.1; -; mRNA.
DR EMBL; AF022138; AAC53494.1; -; mRNA.
DR PIR; JCI1465; JCI1465.
DR Ensembl; ENSRNOG0000020653; Rattus norvegicus.
DR RGD; 68334; Edg5.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IDA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1P_Receptor.
DR Pfam; PF00001; 7tm_1; 1_Receptor.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 34 Extracellular (Potential).
FT TRANSMEM 35 59 1 (Potential).
FT TOPO_DOM 60 66 Cytoplasmic (Potential).
FT TRANSMEM 67 95 2 (Potential).
FT TOPO_DOM 96 109 Extracellular (Potential).
FT TRANSMEM 110 128 3 (Potential).
FT TOPO_DOM 129 147 Cytoplasmic (Potential).
FT TRANSMEM 148 173 4 (Potential).
FT TOPO_DOM 174 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 233 Cytoplasmic (Potential).
FT TRANSMEM 234 255 6 (Potential).
FT TOPO_DOM 256 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT TOPO_DOM 293 352 Cytoplasmic (Potential).
FT LIPID S-palmitoyl cysteine (By similarity).
FT CARBOHYD 19 19 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 89.9%; Score 1625.5; DB 1; Length 352;
Best Local Similarity 89.5%; Pred. No. 5.5e-102;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLSYELNPNKVOEHYNTKETLETQETTSRQVASFIVILCCAIWENLLVLIIVAR 60
DB 1 MGGLSYELNPNKVOEHYNTKETLDMQETPSRKVASAFIILCCAIWENLLVLIIVAR 60

QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
|||||

Db 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLIAIAIERHVAIAKVLGSDKSCRMILLIGASWLSISVLGGLPIGLWNCGLHLEACS 180
|||||
Db 121 FSLIAIAIERHVAIAKVLGSDKSCRMILLIGASWLSISVLGGLPIGLWNCGLHLEACS 180
|||||
QY 181 TVLPLYAKHYVLCVVTIFSIILLAVALYRIYCVVRSHADMAAPOTLALLKTVTVILG 240
|||||
Db 181 TVLPLYAKHYVLCVVTIFSVILLIAVALYRIYFVVRSSHADVAGPOTLALLKTVTVILG 240
|||||
QY 241 VFIVCMLPAPFISILLDYACVPVHSCPIYKAYHLYFAVATLSLNPVIYTWRSRLRREVL 300
|||||
Db 241 VFIIICMLPAPFISILLDSTCPVACPVLYKAYHFAFATLSLNPVIYTWRSRLRREVL 300
|||||
QY 301 RPLQWRPGVGVQRRGGTTPGHLLPLRSSSSSLERGMHMTPTTFLEGNTVV 353
|||||
Db 301 RPLLQWRQKRGATG-RRGGNPGHRLPLRSSSSSLERGLHMTPTTFLEGNTVV 352

RESULT 4
Q54A16 RAT PRELIMINARY; PRT; 352 AA.
ID Q54A16;
AC Q54A16;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AGR16.
GN Name=AGR16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
EX MEDLINE=93176155; PubMed=8382486;
RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
RA Takawa Y.;
RT "Molecular cloning of a novel putative G protein-coupled receptor
RT expressed in the cardiovascular system";
RL Biochem. Biophys. Res. Commun. 190:1104-1109(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RA Gonda K., Takawa Y.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AB016931; BAA32454.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR004063; EDG5_Receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1P_Receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 89.9%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 5.5e-102;
Matches 316; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLSYELNPNKVOEHYNTKETLETQETTSRQVASFIVILCCAIWENLLVLIIVAR 60
DB 1 MGGLSYELNPNKVOEHYNTKETLDMQETPSRKVASAFIILCCAIWENLLVLIIVAR 60

QY 61 NSKFHSAWYLFGLNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
|||||

DB 61 NSKFSHMYFLGNLAASDLLAGVAVFVANTLLSGPVTLSLTPLOWFAREGSAFILTASV 120
 QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGLPILGWNCLHLEACS 180
 DB 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGLPILGWNCLHLEACS 180
 QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVAVYVRIYCVVRSRSHADMAAPQTLALKTTIVLG 240
 DB 181 TVPLPYAKHYVLCVVTIFSVILLATVALVYVYVRSRSHADVAGPQTALLKTTIVLG 240
 QY 241 VPIVWLPFAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVYVYVRSRDRRREVL 300
 DB 241 VPIICWLPFAFSLILLDSTCPVRACPVLYKAHYFFAFATLNSLNPVYVYVRSRDRRREVL 300
 QY 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGMHMTSPTFLEGNTVV 353
 DB 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGMHMTSPTFLEGNTVV 352

RESULT 5
 EDG5_MOUSE STANDARD; PRT; 352 AA.
 AC P52592; Q9R236;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
 DE (lysophospholipid receptor B2) (Endothelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2).
 GN Name=Edg5; Synonyms=Gpcr13, Lpb2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RX NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
 [1]
 RP STRAIN=129/SvJ;
 RC MEDLINE=99132320; PubMed=9931453; DOI=10.1016/S0378-1119(98)00589-7;
 RA Zhang G., Contos J.J.A., Weiner J.A., Fukushima N., Chun J.;
 RT "Comparative analysis of three murine G-protein coupled receptors activated by sphingosine-1-phosphate.";
 RL Gene 227:89-99(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE OF 62-241.
 RC TISSUE=Testis;
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I., Copeland N.G., Jenkins N.A.;
 RA "Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptors.";
 RL Genomics 18:175-184(1993).
 CC -1- FUNCTION: Receptor for the lysophospholipid sphingosine 1-phosphate (S1P). S1P is a bioactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Most abundant in heart and lung; low, but clearly observed in kidney, liver and thymus; much lower but detectable in brain, testis, stomach and intestine. Not significantly detected in any of the sections of embryonic day (E) 14-18, except in embryonic brain.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 CC -----
 CC EMBL; AF108020; AAD16976.1; -; Genomic DNA.
 CC EMBL; L20334; AAI16846.1; -; mRNA.
 CC PIR; E48909; E48909.
 CC Ensembl; ENSMUSG00000043895; Mus musculus.

DR MGI; MGI:99569; Edg5.
 DR GO; GO:0007610; P:behavior; IMP.
 DR InterPro; IPR004063; EDG5_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR004061; S1P_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01525; EDG5RECEPTOR.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PRINTS; PR01523; S1PRECEPTOR.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; PARTIAL.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
 FT TOPO_DOM 1 34 Extracellular (Potential).
 FT TRANSMEM 35 59 1 (Potential).
 FT TOPO_DOM 60 66 Cytoplasmic (Potential).
 FT TRANSMEM 67 95 2 (Potential).
 FT TOPO_DOM 96 109 Extracellular (Potential).
 FT TRANSMEM 110 128 3 (Potential).
 FT TOPO_DOM 129 147 Cytoplasmic (Potential).
 FT TRANSMEM 148 173 4 (Potential).
 FT TOPO_DOM 174 189 Extracellular (Potential).
 FT TRANSMEM 190 210 5 (Potential).
 FT TOPO_DOM 211 233 Cytoplasmic (Potential).
 FT TRANSMEM 234 255 6 (Potential).
 FT TOPO_DOM 256 271 Extracellular (Potential).
 FT TRANSMEM 272 292 7 (Potential).
 FT TOPO_DOM 293 305 Cytoplasmic (Potential).
 FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 19 19 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 166 166 P -> S (in Ref. 2).
 FT CONFLICT 175 175 Q -> K (in Ref. 2).
 FT CONFLICT 189 189 H -> R (in Ref. 2).
 SQ SEQUENCE 352 AA; 38871 MW; 9A3E456DD488FE6B CRC64;
 Query Match 89.7%; Score 1622.5; DB 1; Length 352;
 Best Local Similarity 89.8%; Pred. No. 8.7e-102;
 Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;
 QY 1 MGSLYSELYNKNQVHNYTKETLTQTSRQVASFIVILCCAIWVNLVLIAR 60
 DB 1 MGSLYSELYNKNQVHNYTKETLTQTSRQVASFIVILCCAIWVNLVLIAR 60
 QY 61 NSKFSHMYFLGNLAASDLLAGVAVFVANTLLSGVTLRLTPVQFAREGSAFILTASV 120
 DB 61 NSKFSHMYFLGNLAASDLLAGVAVFVANTLLSGVTLRLTPVQFAREGSAFILTASV 120
 QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGLPILGWNCLHLEACS 180
 DB 121 FSLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGLPILGWNCLHLEACS 180
 QY 181 TVPLPYAKHYVLCVVTIFSIILLAVVAVYVRIYCVVRSRSHADMAAPQTLALKTTIVLG 240
 DB 181 TVPLPYAKHYVLCVVTIFSVILLATVALVYVYVRSRSHADVAGPQTALLKTTIVLG 240
 QY 241 VPIVWLPFAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVYVYVRSRDRRREVL 300
 DB 241 VPIICWLPFAFSLILLDSTCPVRACPVLYKAHYFFAFATLNSLNPVYVYVRSRDRRREVL 300
 QY 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGMHMTSPTFLEGNTVV 353
 DB 301 RPLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGMHMTSPTFLEGNTVV 352

RESULT 6
 EDG5_BRARE STANDARD; PRT; 370 AA.
 AC Q918K8;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
 DE (Sphingosine 1-phosphate receptor 2) (S1P2).
 DE

GN Name=edg5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS MIL HIS-150 AND CYS-167.
RX MEDLINE=20365730; PubMed=10910360; DOI=10.1038/35018092;
RA Kupperman E., An S., Osborne N., Waldron S., Stanner D.Y.R.;
RT "A sphingosine-1-phosphate receptor regulates cell migration during
RT vertebrate heart development.";
RL Nature 406:192-195(2000).
CC -!- FUNCTION: Receptor for the lysophospholipid sphingosine 1-
CC phosphate (S1P). S1P receptor is critical for cell migration and
CC epithelial integrity during vertebrate embryogenesis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: The expression pattern is complex and
CC dynamic. Maternal expression is found in a diffuse pattern
CC throughout the blastoderm, and this pattern persists through the
CC onset of gastrulation. More pronounced expression can be seen at
CC tailbud stage in the anterior portion of the embryo and along the
CC midbrain/hindbrain boundary and the tip of the tail where blisters
CC later develop in receptor mutants. At the 18-somite stage,
CC expression appears just lateral to the midline, and as the
CC myocardial precursors migrate to the midline, their location
CC overlaps with this domain of receptor expression.
CC -!- DISEASE: Defects in edg5 are a cause of heart development
CC abnormality named miles apart (mil). In all vertebrates, the
CC myocardial progenitors involute early during gastrulation and come
CC to occupy bilateral positions in the anterior lateral plate
CC mesoderm (lPM). During somitogenesis, these cells undergo a second
CC phase of migration toward the midline and fuse to form the
CC definitive heart tube. Defects in EDG5 disrupt this process,
CC leading to the formation of two laterally positioned hearts
CC (cardia bifida). The mil phenotype for which two recessive alleles
CC exist, mil(m93) and mil(te273) are fully penetrant.
CC mil(m93)/mil(te273) transheterozygous embryos display the same
CC phenotype as homozygotes for either single mutant allele. In
CC addition to cardia bifida, mil mutants display epithelial tail
CC blisters, indicative of a defect in epithelial integrity.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL, AF260256; AAF88001.1; -, mRNA.
CC ZFIN, ZDB-GENE-020123-2; edg5.
CC DR Ensembl; ENSDARG0000009719; Danio rerio.
CC DR InterPro; IPR000987; EDG1receptor.
CC DR InterPro; IPR000276; GPCR_Rhodpsn.
CC DR InterPro; IPR004061; S1P_receptor.
CC DR Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00642; EDG1RECEPTOR.
CC DR PRINTS; PR00237; GPCR_RHODOPSIN.
CC DR PRINTS; PR01523; S1PRECEPTOR.
CC DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
CC DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
KW Disease mutation; G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 57 Extracellular (Potential).
FT TRANSMEM 58 78 1 (Potential).
FT TOPO_DOM 79 87 Cytoplasmic (Potential).
FT TRANSMEM 88 108 2 (Potential).
FT TOPO_DOM 109 128 Extracellular (Potential).
FT TRANSMEM 129 149 3 (Potential).
FT TOPO_DOM 150 167 Cytoplasmic (Potential).
FT TRANSMEM 168 188 4 (Potential).
FT TOPO_DOM 189 214 Extracellular (Potential).

FT TRANSMEM 215 235 5 (Potential).
FT TOPO_DOM 236 254 Cytoplasmic (Potential).
FT TRANSMEM 255 275 6 (Potential).
FT TOPO_DOM 276 289 Extracellular (Potential).
FT TRANSMEM 290 310 7 (Potential).
FT TOPO_DOM 311 370 Cytoplasmic (Potential).
FT LIPID 325 325 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 24 24 N-linked (GlcNAc...) (potential).
FT VARIANT 150 150 R -> H (in mil; allele m93; lack of S1P-mediated signaling).
FT VARIANT 167 167 R -> C (in mil; allele te273; lack of S1P-mediated signaling).
SQ SEQUENCE 370 AA; 41777 MW; 8C6B3A06DEEA6757 CRC64;

Query Match 55.2%; Score 998; DB 1; Length 370;
Best Local Similarity 58.2%; Pred. No. 1.5e-59;
Matches 199; Conservative 52; Mismatches 73; Indels 18; Gaps 4;

QY 3 SLYSEYLNPNKVOHNYTK-----TLEOTTSROVSAFIVILCCAIVVENLLV 54
DB 17 SKYQYFNKLIQVHYITAKMTAEELDRDIESQSLSS--LNLFFVIGSIIIDENLLV 74

QY 55 LIAVARNKSFHSAMYLEFLGNLAADLLAGVAFVANTLLSGSVTLRLTFVQWFAREGSAFI 114
DB 75 LIAVFRNKKFHSAMFFIGNLAPSDLLAGSAYIANIFLSGPRTHLTPVQWFIREGTAFI 134

QY 115 TLSASVFSLLAIAIERHVAITAKVLYGSDKSCRMILLIGASWLSLVGLGPIILGNCLG 174
DB 135 ALSASVFSLLAIAIERHVAITAKVLYGSDKSCRMILLIGASWLSLVGLGPIILGNCLG 194

QY 175 HLEACSTPLIYAKHYVLCVVTIFSIILLAVVALYVRIYCVRSSHADMAAPQTALLKT 234
DB 195 NLDDCSAVLPNTRYIRFVVTIFSIILLAVVALYVRIYCVRSSHADMAAPQTALLKT 254

QY 235 VTIVLGVFICWLPFAFSILLIDYACPVHSCPILYKAHYLFVAVSTLNSLLNPVIYTWRSRD 294
DB 255 VTIVLGVFICWLPFAFSILLIDYACPVHSCPILYKAHYLFVAVSTLNSLLNPVIYTWRSRD 314

QY 295 LRRVLPLOQWRPGVGVQRRGGTGGHH--LPLRSSSSLE 335
DB 315 MRKEFLRVLCW-----GLLNCGRPPHRCVPLKSSSME 349

RESULT 7
Q91XR0_CAVPO PRELIMINARY; PRT; 202 AA.
ID Q91XR0_CAVPO PRELIMINARY; PRT; 202 AA.
AC Q91XR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endothelial differentiation sphingolipid G-protein-coupled receptor 5 (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L., Cowles R.A., Turner D.J., Logsdon C.D., Mulholland M.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289992; AAK83087.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007185; P:signal transduction; IEA.
DR InterPro; IPR004063; EDG5_Receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1P_receptor.
DR Pfam; PF00001; 7tm_1; 1.

```
DR PRINTS; PRO1525; EDG5RECEPTOR.
DR PRINTS; PRO0237; GPCRHOPOPSN.
DR PRINTS; PRO1523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; UNKNOWN 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2_1; 1.
KW G-protein coupled receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 21836 MW; D9814EC5842320A CRC64;

Query Match 51.5%; Score 932; DB 2; Length 202;
Best Local Similarity 91.1%; Pred. No. 2.4e-55;
Matches 184; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 20 YKETELETQETTSRQVASFIVLCCAIIVENLLVLIIVARNKSHSAMYLEFLGNLAASD 79
DB 1 YKETELETQETTSRQVASFIVLCCAIIVENLLVLIIVARNKSHSAMYLEFLGNLAASD 60

QY 80 LLAGVAFVANTLLSGSVTLRLTPVOWFAREGSAFVLSASFVSLLAIAIERHVAIAKVKL 139
DB 61 LLAGVAFVANTLLSGSVTLRLTPVOWFAREGSAFVLSASFVSLLAIAIERHVAIAKVKL 120

QY 140 YGSDKSCRMLLIGASWLLVGLGPIILGWNCLEHLEACSTVLPYAKHYVLCVVTIPS 199
DB 121 YGSDKSCRMLLIGASWLLVGLGPIILGWNCLEHLEACSTVLPYAKHYVLCVVTIPS 180

QY 200 IILLAVVALYVRIYCVRRSSHA 221
DB 181 VILLAIWVLYVRIYCVRRSSHA 202

RESULT 8
Q9ESKO RAT PRELIMINARY; PRT; 190 AA.
AC Q9ESKO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2003 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative G-protein coupled receptor (Fragment).
GN Name=GPCR18;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley/Hsd;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004063; EDG5 receptor.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR004061; S1P_receptor.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PRO1525; EDG5RECEPTOR.
DR PRINTS; PRO0237; GPCRHOPOPSN.
DR PRINTS; PRO1523; S1PRECEPTOR.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2_1; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 190
SQ SEQUENCE 190 AA; 20718 MW; 3CA0A5C188E168B1 CRC64;

Query Match 48.0%; Score 869; DB 2; Length 190;
Best Local Similarity 88.4%; Pred. No. 4.1e-51;
Matches 168; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 94 GSVTLRLTPVQWFAREGSAFVLSASFVSLLAIAIERHVAIAKVKLYGSDKSCRMLLIG 153
DB 1 GSVTLRLTPVQWFAREGSAFVLSASFVSLLAIAIERHVAIAKVKLYGSDKSCRMLLIG 60

QY 154 ASWLSLVGLGPIILGWNCLEHLEACSTVLPYAKHYVLCVVTIPSILLAVVALYVRIY 213
DB 61 ASWLSLVGLGPIILGWNCLEHLEACSTVLPYAKHYVLCVVTIPSILLAVVALYVRIY 120

QY 214 CVVRSSHADMAAPQTLALLKTKVTIVLGVFVLCWLPAPSFILLLDVACPVHSCPILYKAHYL 273
DB 121 FVVRSSHADVAGPQTLALLKTKVTIVLGVFVLCWLPAPSFILLLDVACPVHSCPILYKAHYL 180

QY 274 FAVSTLNSLL 283
DB 181 FAFATLNSLL 190

RESULT 9
Q5R7A1 PONPY PRELIMINARY; PRT; 382 AA.
AC Q5R7A1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469M1119.
GN Name=DKFZp469M1119;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RC The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; CR860217; CAH92359.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000987; EDG1receptor.
DR InterPro; IPR002277; EDG2 receptor.
DR InterPro; IPR004061; S1P_receptor.
DR InterPro; IPR004061; S1P_receptor.
DR PANTHER; PTHR19286:SF5; EDG1receptor; 1.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PRO0642; EDG1RECEPTOR.
DR PRINTS; PRO1148; EDG2RECEPTOR.
DR PRINTS; PRO0237; GPCRHOPOPSN.
DR PRINTS; PRO1523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2_1; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
SQ SEQUENCE 382 AA; 42773 MW; 6F0841D0E93789CC CRC64;

Query Match 47.3%; Score 856; DB 2; Length 382;
Best Local Similarity 51.1%; Pred. No. 5.9e-50;
Matches 161; Conservative 59; Mismatches 83; Indels 12; Gaps 2;

QY 3 SLYSEVLPNKVQEHYNYT-KETLETOETTSRQVASFIVLCCAIIVENLLVLIIVARN 61
DB 14 SSVSDYVNDYIIVRYNYTKLNISADKENSIKLTSVWFILICCFILNIFVLLTKWT 73

QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFVLSASFV 121
DB 74 KKFHRPMYFIIGNLALSDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFVLSASFV 133
```


NCBI_TaxID=10116;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Cerebellum;
RX MEDLINE=95047498; PubMed=7959012; DOI=10.1016/0378-1119(94)90171-6;
RA Lado D.C., Browe C.S., Gaskin A.A., Borden J.M., MacLennan A.J.;
RT "Cloning of the rat edg-1 immediate-early gene: expression pattern
suggests diverse functions.";
RL Gene 149:331-336(1994).
CC -1- FUNCTION: Receptor for the lysophospholipid sphingosine 1-
phosphate (S1P). S1P is a bioactive lysophospholipid that elicits
diverse physiological effect on most types of cells and tissues.
CC This inducible epithelial cell G-protein-coupled receptor may be
involved in the processes that regulate the differentiation of
endothelial cells. Seems to be coupled to the G(i) subclass of
heteromeric G proteins (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DEVELOPMENTAL STAGE: First detected at embryonic day 15. At
postnatal day 14 detected in skin, spleen, liver, kidney, heart,
testicle, lung and brain. At adulthood is most abundant in brain.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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at the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL: U10303; AAA83418.1; -; mRNA.
CC F1R: I53870; I53870.
CC RGD: G1958; Edg1.
CC GO: GO:0004930; F:G-protein coupled receptor activity; TAS.
CC GO: GO:0045446; P:endothelial cell differentiation; IEP.
CC GO: GO:0030182; P:neuron differentiation; IEP.
CC GO: GO:0019226; P:transmission of nerve impulse; IEP.
CC InterPro: IPR000987; EDG1receptor.
CC InterPro: IPR002277; EDG2 receptor.
CC InterPro: IPR000276; GPCR Rhodopsin.
CC InterPro: IPR004061; S1P Receptor.
CC PANTHER: PTHR19266:SP5; EDG1receptor; 1.
CC Pfam: PF00001; 7tm1; 1.
CC PRINTS: PR00642; EDG1RECEPTOR.
CC PRINTS: PR01148; EDG2RECEPTOR.
CC PRINTS: PR00237; GPCR RHODOPSIN.
CC PRINTS: PR01523; S1PRECEPTOR.
CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW phosphorylation; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 47 Extracellular (Potential).
FT TRANSMEM 48 72 1 (Potential).
FT TOPO_DOM 73 79 Cytoplasmic (Potential).
FT TRANSMEM 80 108 2 (Potential).
FT TOPO_DOM 109 122 Extracellular (Potential).
FT TRANSMEM 123 141 3 (Potential).
FT TOPO_DOM 142 160 Cytoplasmic (Potential).
FT TRANSMEM 161 186 4 (Potential).
FT TOPO_DOM 187 202 Extracellular (Potential).
FT TRANSMEM 203 223 5 (Potential).
FT TOPO_DOM 224 257 Cytoplasmic (Potential).
FT TRANSMEM 258 279 6 (Potential).
FT TOPO_DOM 280 295 Extracellular (Potential).
FT TRANSMEM 296 316 7 (Potential).
FT TOPO_DOM 317 383 Cytoplasmic (Potential).
FT MOD_RES 354 354 Phosphoserine (Potential).
FT LIPID 329 329 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 31 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 383 AA; 42746 MW; 090BA6AE09D34F3 CRC64;
Query Match 46.8%; Score 847; DB 1; Length 383;
Best Local Similarity 48.4%; Pred. No. 2.4e-49;
Matches 167; Conservative 61; Mismatches 103; Indels 14; Gaps 4;


```
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsumura T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[7]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6; TISSUE=Eye, and Mouse;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[8]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
[9]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AK004591; BAB23393.1; -; mRNA.
DR EMBL; BC049094; AAH49094.1; -; mRNA.
DR EMBL; BC051023; AAH51023.1; -; mRNA.
DR ENSEMBL; ENSMUSG0000045092; Mus musculus.
DR MGI; MGI:1096355; Edg1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0001525; P:angiogenesis; IDA.
DR GO; GO:0007193; P:G-protein signaling, adenylyate cyclase inhi. . .; IDA.
DR GO; GO:0030155; P:regulation of cell adhesion; IDA.
DR InterPro; IPR000987; EDG1receptor.
DR InterPro; IPR002277; EDG2 receptor.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR InterPro; IPR004061; S1P receptor.
DR PANTHER; PTHR19266:SF5; EDG1receptor; 1.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00642; EDG1RECEPTOR.
DR PRINTS; PR01146; EDG2RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G PROTEIN RECEPTOR.
DR PROSITE; PS0262; G PROTEIN RECEPTOR.
DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 382 AA; 42639 MW; 5FE4C9A2BD5632A CRC64;
```

```
Query Match 46.7%; Score 845; DB 2; Length 382;
Best Local Similarity 48.4%; Pred. No. 3.3e-49;
Matches 167; Conservative 61; Mismatches 103; Indels 14; Gaps 4;

QY 3 SLYSEYLPNPKVQEHYNT-KETLETQTTTSRQVASAFIVLCCAIVVENLLVLIATVARN 61
DB 14 SSVSDYGYNDIYVRHYNTGKLTGAEKDHGKLVVFIICCFIILENIPVLLTIWKT 73
QY 62 SKFHSAMYLFGLNLAASDLLAGVAVANTLLSGVTSVLTLPVQVFAFGSFAFITSASVF 121
DB 74 KKFHRPMYFIONLALSLLAGVATYANLLSGATYKLTQAQWFLRGSMEVALSASFV 133
QY 122 SLLAIAIERHVAIAKVLYGSDKSCRMILLIGASMLISLVGLGGLPILGNWCLHLEACST 181
DB 134 SLLAIAIERIYITMLKQMLHNGSNSRSLISACWVISLILGGLPIMGNWNCISSSCST 193
QY 182 VLPLYAKHYVLCVVTIFSIILLAVVLYVRYCVRS-----SHADMAAPQTLA 230
DB 194 VLPLYKHVILFCTVFTLLLSIVLYCRYSLVTRSRRLTFRKNISKASRSSEKSLA 253
QY 231 LLKTVTVILGVFIWCVLPAPFSLILLDYACPVHSCPIYKAHYLEAVSTLSLNPVIYTW 290
DB 254 LLKTVTVILSVFIACWAPLFIILLDVGCKKATCDILYKAEFLVLAUNSGTNFIYTL 313
QY 291 RSRDLRRRLRPLQCRW-PGVGVQGR-RRGGTTPGHLLPLRSSSS 333
DB 314 TNKENRAFIRVSCCKCPNGSDSACKFKRPIIPGMFEFSRKSNDNS 358

RESULT 14
Q5BIP0 BOVIN PRELIMINARY; PRT; 382 AA.
AC Q5BIP0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Endothelial differentiation, sphingolipid G-protein-coupled receptor,
DE 1.
GN Name=EDG1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grose W.M., Freking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Perteau G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RA Harhay G.P., Sonstegard T.S., Van Tassel C.P., Clawson M.L.,
RA Heaton M.P., Keele J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; BT021184; AAX31366.1; -; mRNA.
DR EMBL; BT021154; AAX31336.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 4, 2005, 06:38:17 ; Search time 24.5 Seconds
(without alignments)
1386.307 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLYSEYLNPNKQVQEHYNY.....LARGMHMPTSPTFLEGNVTW 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1625.5	89.9	352	JC1465	probable G protein
2	847	46.8	383	I53870	Edg-1 orphan recep
3	836.5	46.2	381	A35300	G protein-coupled
4	817.5	45.2	362	JC7559	sphingosine 1-phos
5	808	44.7	180	E48909	G protein-coupled
6	769	42.5	378	JC5245	G protein-coupled
7	506	28.0	364	JC5293	lysophosphatidic a
8	352.5	19.5	323	S43850	melanocortin 3 rec
9	348.5	19.3	360	B46647	melanocortin recep
10	348	19.2	362	I65990	G protein-coupled
11	345	19.1	330	A55689	G protein-coupled
12	339.5	18.8	363	S48697	probable G protein
13	338.5	18.7	323	S36636	melanocortin recep
14	336	18.6	330	S40454	G protein-coupled
15	305	16.9	325	JC2193	melanocortin recep
16	302	16.7	372	I49008	melanocortin-5 rec
17	301.5	16.7	314	S71420	melanocortin 1 rec
18	300	16.6	473	A33117	cannabinoid recep
19	299.5	16.6	332	A57055	melanocortin recep
20	295.5	16.3	325	JC5592	melanocortin 5 rec
21	291.5	16.1	325	JN0764	melanocortin recep
22	290.5	16.1	347	S70364	cannabinoid recep
23	290	16.0	317	S45708	MSH receptor - bov
24	288.5	15.9	314	S70005	melanocortin 1 rec
25	286	15.8	472	S17595	cannabinoid recep
26	285	15.8	315	S25581	melanocyte-stimula
27	284.5	15.7	317	T12055	melanocyte stimula
28	284.5	15.7	412	A48978	adenosine receptor
29	284	15.7	360	S36750	cannabinoid recep

30	282	15.6	410	2	A48974	adenosine receptor
31	280.5	15.5	320	2	S18444	G protein-coupled
32	279.5	15.5	409	2	I48095	A2 adenosine recep
33	277	15.3	317	2	S29204	melanotropin recep
34	275.5	15.2	325	2	I46416	melanocyte-stimula
35	272	15.0	296	2	I52326	adrenocorticotropi
36	271	15.0	296	2	JC4046	adrenocorticotropi
37	271	15.0	501	2	JH0447	alpha-1A-adrenergic
38	271	15.0	572	2	I39369	alpha-1A-adrenergic
39	270.5	15.0	412	2	D30341	G protein-coupled
40	267	14.8	515	2	A40491	alpha-1-adrenergic
41	263	14.5	560	2	A38731	alpha-1A adrenergic
42	261.5	14.5	297	2	C43265	adrenocorticotropi
43	258.5	14.3	409	2	S68247	adenosine A2a rece
44	255	14.1	387	2	S55550	5-HT4S receptor -
45	255	14.1	406	2	S55549	serotonin 4 recept

ALIGNMENTS

RESULT 1

JC1465
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JC1465
R:Okazaki, H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa, Y
Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993
A:Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in t
A:Reference number: JC1465; MUID:93176155; PMID:8382486
A:Accession: JC1465
A:Molecule type: mRNA
A:Residues: 1-352 <OKA>
A:Cross-references: UNIPROT:P47752; UNIPARC:UPI000000007D; GB:AB016931; NID:93445557; P1
A:Experimental source: aortic smooth muscle
C:Superfamily: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
C:Keywords: G protein-coupled receptor; glycoprotein; glycosylated <TM1>
F:35-59/Domain: transmembrane #status predicted <TM2>
F:67-95/Domain: transmembrane #status predicted <TM2>
F:110-128/Domain: transmembrane #status predicted <TM3>
F:148-173/Domain: transmembrane #status predicted <TM4>
F:190-210/Domain: transmembrane #status predicted <TM5>
F:234-255/Domain: transmembrane #status predicted <TM6>
F:272-293/Domain: transmembrane #status predicted <TM7>
F:19/Binding site: carboxylate (Asn) (covalent) #status predicted
F:142,145,218,219,329,330,331,332/Binding site: phosphate (Ser) (covalent) #status predi
F:313/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match	89.9%	Score	1625.5	DB 2	Length	352			
Best Local Similarity	89.5%	Pred. No.	6.3e-125						
Matches	316	Conservative	14	Mismatches	22	Indels	1	Gaps	1
Qy	1	MGSLYSEYLNPNKVOEHYNTYKTELETOETTSRQVASAFIVILCCAIWENLLVIAVAR	60						
Db	1	MGGLYSEYLNPEKVOEHYNTYKTELDQETPSRKVASAFIILCCAIWENLLVIAVAR	60						
Qy	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV	120						
Db	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASV	120						
Qy	121	FSLLAIAIERHVAIAKVKLYGSKDSCRMILLIGASWLSLVLGGLPILGNWCLHLEACS	180						
Db	121	FSLLAIAIERQVAIAKVKLYGSKDSCRMILLIGASWLSLVLGGLPILGNWCLHLEACS	180						
Qy	181	TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG	240						
Db	181	TVLPLYAKHYVLCVVTIFSVILLAIVALYVRIYVVRSSHADVAGPQTALLKTKVTIVLG	240						
Qy	241	VFIVCWLPAFSLILLDYACPVHSCFIILYKHYLFAVSTLNSLLNPVIYVWTSRDLRREVL	300						
Db	241	VFIICWLPAFSLILLDSTCPVRCAPVLYKHYFFAFATLNSLLNPVIYVWTSRDLRREVL	300						

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Qy 301 RPLQWRPGVGQRRRGTTGHHLLPLRSSSSSLRGHMPSTPTFLEGNTVV 353
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 RPLLCWRQKGATG-RRGNFGHRLPLRSSSSSLERGLHMPSTPTFLEGNTVV 352

RESULT 2
153870
Edg-1 orphan receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I53870
R:Lado, D.C.; Browe, C.S.; Gaskin, A.A.; Borden, J.M.; MacLennan, A.J.
Gene 149, 331-336, 1994
A:Title: Cloning of the rat edg-1 immediate-early gene: expression pattern suggests dive
A:Reference number: I53870; MUID:95047498; PMID:7955012
A:Accession: I53870
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-383 <RES>
A:Cross-references: UNIPROT:P48303; UNIPARC:UPI0000129BD0; EMBL:U10303; NID:g595396; PID
C:Superfamily: G protein-coupled receptor edg-1

Query Match 46.8%; Score 847; DB 2; Length 383;
Best Local Similarity 48.4%; Pred. No. 1.6e-61;
Matches 167; Conservative 61; Mismatches 103; Indels 14; Gaps 4;

Qy 3 SLYSEYLNPNKVOEHYNYT-KETLETQETTTSRQVASAFIVILCCAIIVENLLVLIARVN 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 SQVSDYGNVDIIVRHVNYTGKLNIGVGHGKLTSSVVFILICCLILENIFVLLTWT 74

Qy 62 SKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFILTASVF 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 KKFHRPMYFYFIGNLALSDDLAVATNALLSGATYKLTQAQWFLREGSMFVALSASF 134

Qy 122 SLLAIAIERHVAIAKVKYGSCKSRMLLIGASWLSLVGLGPILGWNCGLHLEACST 181
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 135 SLLAIAIERYITMLKMKLHNGSNRSRFLLSACWVISLILGGLPIMGWNCISLSSCST 194

Qy 182 VLPLYAKHYVLCVVTIFSIILLAVVALVRYIYCVRS-----SHADMAAPQTLA 230
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 VLPLVHKHYILFCTVTFVLLLSIVILYCRISLVTRSRRLTFRKNISKASRSSEKSLA 254

Qy 231 LLKTTIIVLGVFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLSNLLNPVIYTW 290
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 LLKTTIIVLVSFIACWAPLFLILLDVGCKAKTCDILYKAYFLVLAIVNGTNPVIYTL 314

Qy 291 RSRDLRRLVPLQWR-PGVGVQGR-RRGTPGHLLPLRSSSS 333
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 TNKEMRRAFIRIISCKCPNGDSAGKPKRPIIPGMEFSRSKSDNS 359

RESULT 3
A35300
G protein-coupled receptor edg-1 - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A35300
R:Hla, T.; Maciag, T.
J. Biol. Chem. 265, 9308-9313, 1990
A:Title: An abundant transcript induced in differentiating human endothelial cells encod
A:Reference number: A35300; MUID:90264425; PMID:2160972
A:Accession: A35300
A:Molecule type: mRNA
A:Residues: 1-381 <HLA>
A:Cross-references: UNIPROT:P21453; UNIPARC:UPI0000037801; GB:M31210; NID:g181948; PIDN:
C:Genetics:
A:Gene: GDB:ECGF1
A:Cross-references: GDB:127754; OMIM:131222
A:Map position: 22q13-22q13
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
Query Match 46.2%; Score 836.5; DB 2; Length 381;
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Best Local Similarity 49.7%; Pred. No. 1.2e-60;
Matches 156; Conservative 60; Mismatches 87; Indels 11; Gaps 2;

Qy 3 SLYSEYLNPNKVOEHYNYT-KETLETQETTTSRQVASAFIVILCCAIIVENLLVLIARVN 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 14 SSVSDYVNYDIIIVRHVNYTGKLNISADKENSILKTSVVFILICCFILLENIFVLLTWT 73

Qy 62 SKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFILTASVF 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 KKFHRPMYFYFIGNLALSDDLAVATNALLSGATYKLTQAQWFLREGSMFVALSASF 133

Qy 122 SLLAIAIERHVAIAKVKYGSCKSRMLLIGASWLSLVGLGPILGWNCGLHLEACST 181
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 SLLAIAIERYITMLKMKLHNGSNRFLLSACWVISLILGGLPIMGWNCISLSSCST 193

Qy 182 VLPLYAKHYVLCVVTIFSIILLAVVALVRYIYCVRS-----APQTLAL 231
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 194 VLPLYKHYILFCTVTFVLLLSIVILYCRISLVTRSRRLTFRKNISKASRSSEKSLA 253

Qy 232 LKTTIIVLGVFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLSNLLNPVIYTW 291
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 254 LKTTIIVLVSFIACWAPLFLILLDVGCKVKTCDILFRAEYFLVLAIVNGTNPVIYTL 313

Qy 292 RSRDLRRLVPLQOC 305
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 NKEMRRAFIRIMSC 327

RESULT 4
JC7559
sphingosine 1-phosphate receptor - zebra fish
N:Alternate names: endothelial differentiation gene 1 receptor
C:Species: Brachydanio rerio (zebra fish)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: JC7559
R:Im, D.S.; Ungar, A.R.; Lynch, K.R.
Biochem. Biophys. Res. Commun. 279, 139-143, 2000
A:Title: Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate receptor
A:Reference number: JC7559; MUID: 20563813; PMID:11112429
A:Accession: JC7559
A:Molecule type: DNA
A:Residues: 1-362 <INA>
A:Cross-references: UNIPROT:Q9DDK4; UNIPARC:UPI00001788F3; GB:AF321294
C:Comment: This receptor, a G protein-coupled receptor, mediates sphingosine 1-phosphate
or also functions in the developing central nervous system in cell proliferation, apopto
C:Genetics:
A:Gene: edg1
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 45.2%; Score 817.5; DB 2; Length 362;
Best Local Similarity 45.4%; Pred. No. 3.9e-59;
Matches 161; Conservative 64; Mismatches 109; Indels 21; Gaps 4;

Qy 14 VOEHYNYTKETLETQETTTSRQVASAFIVILCCAIIVENLLVLIARVNSKPFHSAMYFLG 73
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 IARHNYTFGRKVKHDPGLKADSVFIIVCCFILLENVLVLLTIWTKFKHKPMYFYF 64

Qy 74 NLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFILTASVFLSLLAIAIERHVA 133
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 NLALSDDLAVVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 124

Qy 134 IAKVKLYGSKSCRMILLIGASWLSLVGLGPILGWNCGLHLEACSTVPLVYAKHYVIC 193
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 MLKMKLHNGKTCRVFMLISTVFIAILGLGLPVGWNCIDSNINNCSTVPLVYKAYILF 184

Qy 194 VVTFISILLAVVALVRYIYCVRS-----ADMAAPQTLALLKTTVTVLG 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 CTTVFSVILMAIVLYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIYIY 244

Qy 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYLFAVSTLSNLLNPVIYTWRSRDLRVL 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 CFIACWAPLFLILLDVGCKTLCISLYKAEWFLAVALVNSAMNPLIYTLTNSMERRAFI 304
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Query Match      42.5%; Score 769; DB 2; Length 378;
Best Local Similarity 47.2%; Pred. No. 3.6e-55;
Matches 161; Conservative 57; Mismatches 101; Indels 22; Gaps 7;

Qy    14 VQHNYNT-----KETLETTSQVSAFIVILCCAIVENLVLTAVARNKSFHS 66
       :|||   |||   :   :|||:|||||:|||||:|||||:
Db    18 LREHYQYVGKLAKLKEASGSLT----TVLFVICSPVLLENMLVLAIWKNKKFNH 72
       :|||   |||   :   :|||:|||||:|||||:|||||:

Qy    67 AMYLFLGNLAASDLLAGVAFVANVTLLSGSVTLRLTPQWFAREGSAPITLSASFVSLAI 126
       :|||   |||   :   :|||:|||||:|||||:|||||:
Db    73 RMYFFIGNLALCDLLAGIAYKVNIIMGKKTFSLSPTWFLREGSMFVALGASTCSLAI 132
       :|||   |||   :   :|||:|||||:|||||:|||||:

```

```

RESULT 8
S43850
melanocortin 3 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43850; S37153
R:Description: S43850; S37153
R:Desarnaud, F.; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.

```


A;Residues: 1-330 <IIS>
A;Cross-references: UNIPROT:P46089; UNIPARC:UPI0000001624; GB:L32830; GB:L32831; NID:G60
R;Eggenickx, D.; Denef, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, S.; Vassart, G.; Parmant
Biochem. J. 309, 837-843, 1995
A;Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutively a
A;Reference number: S58521; MUID:95366960; PMID:7639700
A;Accession: S58521
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-330 <EGG>
A;Cross-references: UNIPARC:UPI0000001624; GB:X83956; NID:g1061125; PIDN:CAA58787.1; PID
R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, I
Genomics 23, 609-618, 1994
A;Title: Cloning of human genes encoding novel G protein-coupled receptors.
A;Reference number: A55733; MUID:95154831; PMID:7851889
A;Accession: C55733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-292 <MAR>
A;Cross-references: UNIPARC:UPI000016A113; GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:
C;Genetics:
A;Gene: GDB:GPR3
A;Cross-references: GDB:371695; OMIM:600241
A;Map position: lp36.1-lp34.3
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.1%; Score 345; DB 2; Length 330;
Best Local Similarity 33.3%; Pred. No. 1.1e-20;
Matches 96; Conservative 49; Mismatches 107; Indels 36; Gaps 11;

Qy 38 AFIVILCCA---IVVENLLVLIIVARNKSFHSAMYLFLGNLAASDLLAGVAFV---ANTL 91
Db 42 ANDVVLCSGLTVSCENALVVAIVGTAPFAPMFLVGLSLAVADLLAGLGLVLFPAVF 101

Qy 92 LSGSVTLRLTPVQWFAREGSAPITLSASVFSLLAIAIERHVAIAKVLYGSDKS-CRMLL 150
Db 102 CIGSAEMSLVLV-----GVLAWAFTASIGSLLAITVDVRLSYLNALTYSETTTRTVV 155

Qy 151 LIGASWLSLVGLGPIGLWNCGLHLEACSTVPLPYAKHYVLCVVTIFSI---ILLAVVAL 208
Db 156 MLVMYGALGLGLLPVLAWNCLDGLTTCGVVYPLSKNHLVLAIAFFMVFGLMLQLYQA 215

Qy 209 VYRIYCVVRSSHADMAAPQTLAL-----LKTVTIVLGVFIVCWLPAFSILLDY 257
Db 216 ICRIVC-----RHAQIQLQRHLLPASHVATKGIATLAVLGAAPACWLPFTVYCLGD 271

Qy 258 ACPVHSCPILYKAHYLFAVSTLNSLNPVYTWRSRLRREVLRLPQC 305
Db 272 A---HS-PPLY-TYTLTPATYNSMINPIIYAFRNQVQK-VLMAVCC 313

RESULT 12
S48697
probable G protein-coupled receptor protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S48697
R;Song, Z.H.; Young III, W.S.; Brownstein, M.J.; Bonner, T.I.
FEBS Lett. 351, 375-379, 1994
A;Title: Molecular cloning of a novel candidate G protein-coupled receptor from rat brain
A;Reference number: S48697; MUID:94364507; PMID:8082799
A;Accession: S48697
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <SON>
A;Cross-references: UNIPROT:P51651; UNIPARC:UPI000012BA34; EMBL:U12006; NID:g551333; PID
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor

Query Match 18.8%; Score 339.5; DB 2; Length 363;
Best Local Similarity 34.7%; Pred. No. 3.3e-20;
Matches 96; Conservative 51; Mismatches 95; Indels 35; Gaps 12;

Qy 41 VILCCA---IVVENLLVLIIVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLS---G 94
Db 78 VLLCVSGTVIAGENALVVALLIASTPALRTPMFLVGLSATADLLAGCGLLHFVQYVVP 137

Qy 95 SVTLRLTPVQWFAREGSAPITLSASVFSLLAIAIERHVAIAKVLYGSDKS-CRMLLIG 153
Db 138 SETVSLLMV-----GFLVASFAASVSLLAITVDVRLSYLNALTYSSRRLTLLGVHLLA 191

Qy 154 ASWLSISVLGGLPILGWNCLHLEACSTVPLPYAKHYVLCVVTIFSIILLAVVALYRIY 213
Db 192 ATWTVSLGLGLPILGWNCLADRSASVVRLETRSHVAL-LSTSEFFVFGIMLHLVRI- 249

Qy 214 CVVRSSHAD-----MAAPQTLALLK---TVTIVLGVFIVCWLPAFSIILLDYACPVH 262
Db 250 QGVVWRHAHQIALQOCHCLAPPLAATRAKGVGTAAVLGTGFCASWLP-PAIY-----CVVG 303

Qy 263 S---CPILYKAHYLFAVSTLNSLNPVYTWRSRLR 297
Db 304 SQEDPAIY-TYATLLPATYNSMINPIIYAFRNQBIQ 339

RESULT 13

S36636

melanocortin receptor 3 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: A48254; S36636

R;Roselli-Rehfuess, L.; Mounjojoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro, J.

Proc. Natl. Acad. Sci. U.S.A. 90, 8856-8860, 1993

A;Title: Identification of a receptor for gamma melanotropin and other proopiomelanocort

A;Reference number: A48254; MUID:94022273; PMID:8415620

A;Accession: A48254

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-323 <ROS>

A;Cross-references: UNIPROT:P32244; UNIPARC:UPI000012ED4C; EMBL:X70667; NID:g396551; PID

A;Note: submitted to the EMBL Data Library, January 1993

A;Note: in Genbank entry RRM33RA, release 113.0, the source is designated as Rattus ratt

C;Genetics:

A;Gene: MC3-R

C;Superfamily: melanocortin receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.7%; Score 338.5; DB 2; Length 323;

Best Local Similarity 32.1%; Pred. No. 3.5e-20;

Matches 95; Conservative 56; Mismatches 104; Indels 41; Gaps 11;

Qy 41 VILCCAIV---VENLLVLIIVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLL-----S 93

Db 44 VFLALGIVSLMENTILVILAVVRNGLHSPMYFFLLSLLOADMLVLSLSLETIMIVINS 103

Qy 94 GSVTLRLTPVQWFAREGSAPITLSASVFSLLAIAIERHVAIAKVLYGSDKSCRMILL 151

Db 104 DSLTLEDOFIQHMNDIIFDSMICISLVASICNLLAIAVDVYVTFYALRYHSTMTVRKAL- 162

Qy 152 IGASWLSLVGLGPIGLWNCGLHLEACSTVPLPY--AKHYVLCVVTIFSIILLAVVALY 209

Db 163 ---SLIVAI-----WVCCG---ICGVNFIVYSESKMVICLITMFFAMVLLMGTL 207

Qy 210 VRIYCVVR-----SSHADMAAPQTLALLK---TVTIVLGVFIVCWLPAFSILLDYA 258

Db 208 IHMFLFARLHVQRTAALPPADGVAPQHQSHCKGAVTITILGVFFCHWAPFLHLVLIIT 267

Qy 259 CPVHSCPILYKAHY--LFAVSTLNSLNPVYTWRSRLRREVLRLPQCRPGVGV 312

Db 268 CPTNPYCICTAHENTYVLVLMCNVIDPLIYAFRSLEL-RNTPKELICGCGNMV 322

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:24:31 ; Search time 130 Seconds
(without alignments)
1193.082 Million cell updates/sec

Title: US-10-084-507B-22
Perfect score: 1809
Sequence: 1 MGSLSYSEYLNPNKQEHYNY.....LERGMHMTPTFLEGNTVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1809	100.0	353	2	AAY28289 EDG-4 ami
2	1804	99.7	353	2	AAY49904 Human EDG
3	1803	99.7	353	2	AAY28288 Predicted
4	1787	98.8	353	3	AAB18889 Amino aci
5	1787	98.8	353	6	ABP59285 Human Edg
6	1787	98.8	353	6	ABP59285 Human Edg
7	1787	98.8	353	6	ABU08813 Human Edg
8	1787	98.8	353	6	ABP82010 Human sph
9	1787	98.8	353	7	ADC40485 Protein o
10	1787	98.8	353	7	ADD11247 Human Edg
11	1787	98.8	353	7	ADD90760 Human Edg
12	1787	98.8	353	8	ADH57161 Human end
13	1787	98.8	353	8	ADJ62652 Human end
14	1787	98.8	353	8	ADQ29293 Human GPC
15	1787	98.8	353	8	ADO57997 Human GPC
16	1787	98.8	353	8	ADO22422 Human G p
17	1787	98.8	353	8	ADP8359 Human EDG
18	1783	98.6	353	2	AAY49905 Human EDG
19	1783	98.6	353	7	ADD11249 Human EDG
20	1755	97.0	353	9	ADU92079 Human end
21	1631.5	90.2	352	3	AAB03966 Murine ED
22	1625.5	89.9	352	2	AAY58712 Fragment
23	1625.5	89.9	352	2	AAY01663 p(H218),
24	1625.5	89.9	352	2	AAY05492 Human EDG

25	1625.5	89.9	352	2	AAW87790 Rat H218,
26	1625.5	89.9	352	4	AAU00305 LPA recep
27	1625.5	89.9	352	6	ABU07712 Rat lysop
28	1625.5	89.9	352	6	ABP98696 Rat Endot
29	1625.5	89.9	352	7	ABU61816 Human sph
30	1625.5	89.9	352	8	ADP88361 Rat endot
31	1625.5	89.9	353	7	ADD48927 Rat Prote
32	1622.5	89.7	352	8	ABP98695 Murine En
33	1622.5	89.7	352	8	ADO29294 Mouse GPC
34	1509.5	83.4	377	8	ADP29509 Human sec
35	1432	79.2	372	6	ABP59289 Chimeric
36	946	52.3	269	4	ADG15135 Human 7 t
37	946	52.3	274	4	AAW96680 Human rep
38	946	52.3	274	4	ABP96585 Human tes
39	946	52.3	274	4	ADG15162 Human 7 t
40	860.5	47.6	384	6	ABP59281 Chimeric
41	858.5	47.5	384	6	ABP59280 Chimeric
42	858	47.4	391	6	ABP59279 Chimeric
43	854.5	47.2	362	5	ABG75679 Human Edg
44	854.5	47.2	362	8	ADO28787 Arrestin
45	854.5	47.2	362	9	ADX44606 Chimeric

ALIGNMENTS

RESULT 1

RAY28289
ID AAY28289 standard; protein; 353 AA.

XX AAY28289;

DT 12-OCT-1999 (first entry)

DE EDG-4 amino acid sequence encoded by clone pC3-hEDG4#36.

XX EDG-4; polypeptide; receptor; inflammation; amino acid; G protein;

KW lysolipid; immune response.

XX Homo sapiens.

XX WO9935259-A1.

XX 15-JUL-1999.

XX 30-DEC-1998; 98WO-CA001195.

XX 30-DEC-1997; 97US-0070185P.

PR 03-APR-1998; 98US-0080610P.

PR 25-NOV-1998; 98US-0109885P.

PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.

PI Munroe DG, Kamboj R, Peters D, Koosheesh F, Vyas TB, Gupta AK;

XX WPI; 1999-430392/36.

XX New isolated lysolipid/EDG receptor useful in the treatment of asthma and rheumatoid arthritis.

PS Claim 7; Fig 16B; 120pp; English.

CC A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4) . The LL/EDG receptors are involved in an inflammatory response signaling pathway and an apoptotic signaling pathway. They can be used for identifying agonists or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists can be used for upregulation of an inflammatory process condition or immune response. Antagonists can be used for the downregulation of an inflammatory process condition or immune response. The agonists and antagonists can also be used for controlling apoptosis in a cell comprising the LL/EDG receptor. A diagnostic test for aberrant expression of HEDG-4 can accelerate diagnosis and proper treatment of abnormal conditions of e.g. the heart, kidney, lung and testis. Specific examples

CC of conditions in which aberrant expression of HEDG-4 may play a role
CC include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
CC neurotrauma, Alzheimer's disease, endotoxin shock, atherosclerosis,
CC cardiac ischemia, acute pancreatitis, septic shock, pericarditis, acute
CC cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the
CC liver, and early diabetic glomerulopathy, as well as lung damage
CC following exposure to cigarette smoke, asbestos or silica. HEDG-4
CC specific antibodies, inhibitors, ligands or their analogs can be used as
CC bioactive agents to treat inflammation or disease including viral,
CC bacterial or fungal infections, allergic responses, mechanical injury
CC associated with trauma, hereditary diseases, lymphoma or carcinoma, or
CC other conditions which activate the genes of kidney, lung, heart,
CC lymphoid or tissues of the nervous system
XX

SQ Sequence 353 AA;
Query Match 100.0%; Score 1804; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 5,1e-177; Mismatches 0; Gaps 0;
Matches 353; Conservative 0; Indels 0;
QY 1 MGSLYSEYLNPNKQVHEHYNTKETLETTTSRQVASFIVILCCAIIVENLLVLIAR 60
Db |||||
1 MGSLYSEYLNPNKQVHEHYNTKETLETTTSRQVASFIVILCCAIIVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
Db |||||
121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILLAVVLYRIYCVVRSSHADMAAPQTALLKTTVILG 240
Db |||||
181 TVPLYAKHYVLCVVTIFSIILLAVVLYRIYCVVRSSHADMAAPQTALLKTTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDRLRREV 300
Db |||||
241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDRLRREV 300
QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db |||||
301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 2
AA49904
ID AA49904 standard; protein; 353 AA.
AC AA49904;
XX
XX 28-JAN-2000 (first entry)
XX Human EDG family H218 protein.
KW Human; EDG family; H218; transmembrane receptor protein; diagnosis;
KW therapy; bacterial; fungal; viral; infection; HIV; cancer; diabetes;
KW obesity; anorexia; bulimia; asthma; Parkinson's disease; hypotension;
KW acute heart failure; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy;
KW benign prostatic hypertrophy; migraine; vomiting; psychotic;
KW neurological disorder; dyskinesia.
XX
OS Homo sapiens.
XX
XX WO9954351-A1.
XX
XX 28-OCT-1999.
XX
XX 14-APR-1999; 99WO-US008099.
XX
XX 23-APR-1998; 98US-0082776P.
PR
PR 03-SEP-1998; 98US-00150650.

XX (SMIK) SMITHKLINE BEECHAM CORP.
PA Bergsma DU, Elshourbagy N, Lane P, Li X, Mooney JL, Tsui P;
XX
XX WPI, 1999-633972/54.
XX N-PSDB; AAZ32488.
XX
XX Novel human transmembrane receptor protein for use in treatment and
XX diagnosis of disease.
XX
XX Claim 1; Page 29; 49pp; English.

CC The present sequence is a human EDG family protein designated H218. H218
CC is used for diagnosing disease or its susceptibility in a subject related
CC with expression or activity of H218 by determining the presence or
CC absence of mutation in the polynucleotide encoding H218 in the genome of
CC the subject and/or analysing for the presence of H218 expression in
CC sample derived from the subject. It is also used for treating subjects in
CC need of enhanced activity or inhibition of H218 by administering an
CC agonist or antagonist respectively. H218 can be used to treat abnormal
CC conditions such as bacterial, fungal and viral infections, particularly
CC HIV-1 or 2, cancers, diabetes, obesity, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC stroke, ulcers, asthma, allergies, benign prostatic hypertrophy,
CC migraine, vomiting, psychotic, neurological disorders and dyskinesias can
CC be treated. The H218 polynucleotide can also be used for obtaining
CC hybridisation probes and primers for isolating full-length clones
CC encoding H218. The difference in cDNA or genomic sequence between
CC affected and unaffected individuals is determined to identify mutation
CC causing the disease. It is also valuable for chromosome identification.
CC The polypeptide is used for the identification of membrane bound or
CC soluble receptors through standard receptor binding techniques and also
CC for structure based design of agonist, antagonist or inhibitor of the
CC polypeptides
XX

SQ Sequence 353 AA;
Query Match 99.7%; Score 1804; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 1.7e-176;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGSLYSEYLNPNKQVHEHYNTKETLETTTSRQVASFIVILCCAIIVENLLVLIAR 60
Db |||||
1 MGSLYSEYLNPNKQVHEHYNTKETLETTTSRQVASFIVILCCAIIVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
Db |||||
121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILLAVVLYRIYCVVRSSHADMAAPQTALLKTTVILG 240
Db |||||
181 TVPLYAKHYVLCVVTIFSIILLAVVLYRIYCVVRSSHADMAAPQTALLKTTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDRLRREV 300
Db |||||
241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDRLRREV 300
QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db |||||
301 RPLQWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 3
AA49904
ID AA49904 standard; protein; 353 AA.
XX
XX
AC AA49904;

XX 12-OCT-1999 (first entry)
XX Predicted polypeptide product from human EDG-4 cDNA.
XX
XX EDG-4; polypeptide; receptor; inflammation; amino acid; G protein;
XX lysolipid; immune response.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 273 /label= unknown
XX FT /note= "encoded by YTT"
XX
XX WO9935259-A1.
XX
XX 15-JUL-1999.
XX
XX 30-DEC-1998; 98WO-CA001195.
XX
XX 30-DEC-1997; 97US-0070185P.
XX 03-APR-1998; 98US-0080610P.
XX 25-NOV-1998; 98US-0109885P.
XX
XX (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
XX
XX Munroe DG, Kamboj R, Peters D, Kooshesh F, Vyas TB, Gupta AK;
XX
XX WPI; 1999-430392/36.
XX
XX New isolated lysolipid/EDG receptor useful in the treatment of asthma and
XX rheumatoid arthritis.
XX
XX Claim 7; Fig 16A; 120pp; English.
XX
XX A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4). The LL/EDG
XX receptors are involved in an inflammatory response signaling pathway and
XX an apoptotic signaling pathway. They can be used for identifying agonists
XX or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists
XX can be used for upregulation of an inflammatory process condition or
XX immune response. Antagonists can be used for the downregulation of an
XX inflammatory process condition or immune response. The agonists and
XX antagonists can also be used for controlling apoptosis in a cell
XX comprising the LL/EDG receptor. A diagnostic test for aberrant expression
XX of EDG-4 can accelerate diagnosis and proper treatment of abnormal
XX conditions of e.g. the heart, kidney, lung and testis. Specific examples
XX of conditions in which aberrant expression of EDG-4 may play a role
XX include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
XX neurotrauma, Alzheimer's disease, endotoxic shock, atherosclerosis,
XX cardiac ischemia, acute pancreatitis, septic shock, psoriasis, acute
XX cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the
XX liver, and early diabetic glomerulopathy, as well as lung damage
XX following exposure to cigarette smoke, asbestos or silica. EDG-4
XX specific antibodies, inhibitors, ligands or their analogs can be used as
XX bioactive agents to treat inflammation or disease including viral,
XX bacterial or fungal infections, allergic responses, mechanical injury
XX associated with trauma, hereditary diseases, lymphoma or carcinoma, or
XX other conditions which activate the genes of kidney, lung, heart,
XX lymphoid or tissues of the nervous system
XX
XX Sequence 353 AA;
XX
XX Query Match 99.7%; Score 1803; DB 2; Length 353;
XX Best Local Similarity 99.4%; Pred. No. 2.le-176;
XX Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MGSLEYLNPKNVQEHYNTKETLETQETTSRQVASFIVILCCAIVVENLLVIAVAR 60
XX
XX 1 MGSLEYLNPKNVQEHYNTKETLETQETTSRQVASFIVILCCAIVVENLLVIAVAR 60
XX
XX 61 NSKFHSA MYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
XX
XX

Db 61 NSKFHSA MYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLTIGASWLSLVLGGLPILGNWCLHLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLTIGASWLSLVLGGLPILGNWCLHLEACS 180
Qy 181 TVLPIYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
Db 181 TVLPIYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
Qy 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAKHYLFAVSTLNSLLNPVYIWRSDRLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAKHYLFAVSTLNSLLNPVYIWRSDRLRREVL 300
Qy 301 RPLQCRPGVGVQGRRRGTGPHLLPLRSSSSSLERGMHMTPTSFLEGNTVV 353
Db 301 RPLQCRPGVGVQGRRRGTGPHLLPLRSSSSSLERGMHMTPTSFLEGNTVV 353
RESULT 4
AAB18889
ID AAB18889 standard; protein; 353 AA.
XX
XX AAB18889;
XX
XX 08-FEB-2001 (first entry)
XX
XX Amino acid sequence of the human Edg5 polypeptide.
XX
XX Edg4; Edg5; lysophospholipid receptor; sphingolipid receptor; SIP;
XX lysophosphatidic acid; LPA; sphingosine 1-phosphate; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200056135-A2.
XX
XX 28-SEP-2000.
XX
XX 23-MAR-2000; 2000WO-US007649.
XX
XX 23-MAR-1999; 99US-00274752.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Goetzl EI, An S;
XX
XX WPI; 2000-638230/61.
XX N-PSDB; AAA96163.
XX
XX Novel human polypeptide receptors for lysophospholipids and
XX sphingolipids, native human Edg4, Edg5, mutant of Edg4 comprising
XX extended polypeptide tail, used to screen agents that affect LPA and SIP
XX activities.
XX
XX Claim 13; Fig 3; 67pp; English.
XX
XX The present sequence represents an Edg polypeptide. The specification
XX describes Edg4 and Edg5 polypeptides. The Edg4 gene is located on
XX chromosome 19p12. The Edg polypeptides are receptors for
XX lysophospholipids and sphingolipids, such as lysophosphatidic acid (LPA)
XX and sphingosine 1-phosphate (SIP). The Edg receptor proteins are used for
XX diagnosing an LPA or SIP mediator condition an individual. Edg4 and Edg5
XX polypeptides can be used in screening assays designed to determine the
XX effects of a candidate bioactive agent on the expression and activity of
XX Edg4 and Edg5 polypeptides, and the function of LPA and SIP. Nucleotide
XX sequences encoding Edg-4 and Edg-5 are useful as hybridisation probes, in
XX chromosome and gene mapping and in the generation of anti-sense RNA and
XX DNA. Nucleic acids which encode Edg4 or Edg5 or their modified forms can
XX also be used to generate either transgenic animals or knock out animals.
XX Nucleic acid encoding the Edg-4 and Edg-5 polypeptides may also be used
XX in gene therapy
XX
XX Sequence 353 AA;
XX
XX

Query Match 98.8%; Score 1787; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEVLNPNKQOEHNYYTKETLETQETTSROVASAFIVILCCAIWVENLLVLIAR 60
Db 1 MGSLSYSEVLNPNKQOEHNYYTKETLETQETTSROVASAFIVILCCAIWVENLLVLIAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGLPLIGWNCGLHLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGLPLIGWNCGLHLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILLAVALYVRIYCVWRSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAVALYVRIYCVWRSSHADMAAPQTLALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 5
ABP59285
ID ABP59285 standard; protein; 353 AA.

XX AC ABP59285;
XX DT 10-MAY-2003 (first entry)
XX DE Human Edg5 receptor.
XX KW Human; Edg; receptor.
XX OS Homo sapiens.
XX FN WO2003006503-A1.
XX PD 23-JAN-2003.
XX PF 10-JUL-2002; 2002WO-US022346.
XX PR 11-JUL-2001; 2001US-00904099.
XX PA (CERE-) CERETEK.
XX PI Shankar G, Munning JN, Spencer JV;
XX DR WPI; 2003-221718/21.
XX PT New chimeric Edg receptor, useful in high-throughput screening assays,
XX PT comprises extracellular and transmembrane domains of a first Edg
XX PT receptor, and a chimeric intracellular domain of a second Edg receptor.
XX PS Disclosure; Page 19; 71pp; English.
XX CC The present invention relates to Edg receptors (ABP59277-ABP59290). The
XX CC Edg receptors are useful in a high-throughput screening assay to
XX CC identify compounds that bind to or modulate the activity of the
XX CC polypeptide, in calcium mobilisation assays, binding assays, detection of
XX CC cAMP formation, or in reporter gene techniques
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 6; Length 353;

Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEVLNPNKQOEHNYYTKETLETQETTSROVASAFIVILCCAIWVENLLVLIAR 60
Db 1 MGSLSYSEVLNPNKQOEHNYYTKETLETQETTSROVASAFIVILCCAIWVENLLVLIAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGLPLIGWNCGLHLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGLPLIGWNCGLHLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILLAVALYVRIYCVWRSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILLAVALYVRIYCVWRSSHADMAAPQTLALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 6
ABB98694
ID ABB98694 standard; protein; 353 AA.

XX AC ABB98694;
XX DT 10-JAN-2003 (first entry)
XX DE Human Endothelial Differentiation Gene, Edg-5.
XX KW Human; nephrotropic; proliferative glomerular nephritis;
XX KW Endothelial Differentiation Gene; Edg-5; Iga nephritis.
XX OS Homo sapiens.
XX FN WO200277642-A1.
XX PD 03-OCT-2002.
XX PF 25-MAR-2002; 2002WO-JP002828.
XX PR 26-MAR-2001; 2001JP-00088018.
XX PR 06-SEP-2001; 2001JP-00270551.
XX PA (NNSH) NIPPON SHINYAKU CO LTD.
XX PI Takagaki K, Katsuma S, Tsujimoto G;
XX DR WPI; 2003-018956/01.
XX DR N-PSDB; ABQ81030.
XX PT Screening drugs for preventing or treating (mesangial) proliferative
XX PT glomerular nephritis, based on inhibiting activation of Edg-5 for
XX PT particularly Edg-5 receptor antagonists.
XX PS Claim 3; Page 44; 59pp; Japanese.
XX CC The present invention relates to methods for screening for preventives or
XX CC remedies for proliferative glomerular nephritis, depending on the
XX CC inhibitory effect on Endothelial Differentiation Gene, Edg-5, activation.
XX CC The method is especially useful for screening preventives or remedies for
XX CC Iga nephritis. The present sequence is human Edg-5, which was used in the
XX CC method of the invention
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 6; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
DB 1 MGSLEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIWVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCGLHLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRRSHADMAAPQTALLKTVTVILG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRRSHADMAAPQTALLKTVTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTPFLGNTVV 353
DB 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTPFLGNTVV 353

RESULT 7
ABU0813
ID ABU0813 standard; protein; 353 AA.
XX ABU0813;
XX 11-AUG-2003 (first entry)
XX Human EDG-5 protein.
XX Human; lymphocyte activation; lymphocyte migration; EDG-5;
KW G-protein coupled receptor; GPCR; lymphocyte; T cell receptor;
KW B cell receptor; CD69; gene therapy; asthma; allergy; autoimmune disease;
KW multiple sclerosis; scleroderma; pernicious anaemia; IDDM;
KW insulin-dependent diabetes mellitus; tissue transplant;
KW Graft-versus-host disease; inflammation; infection.
XX Homo sapiens.
XX US2002155512-A1.
XX 24-OCT-2002.
XX 03-OCT-2001; 2001US-00971228.
XX 18-APR-2001; 2001US-0284763P.
XX (RIGB-) RIGEL PHARM INC.
XX Liao XC, Masuda E, Chu P, Pardo J, Li C, Zhao H, Jiang Y;
XX WPI; 2003-340852/32.

Identifying lymphocyte modulator activation/migration, by contacting an
PT EDG G-protein coupled receptor polypeptide or cell having the polypeptide
PT with compound and determining chemical/phenotypic effect of compound on
PT cell.
XX
PS Disclosure; Fig 2; 70pp; English.
XX
XX The invention discloses method for identifying a compound that modulates
CC lymphocyte activation/migration. The method comprises contacting an EDG G
CC -protein coupled receptor (GPCR) family polypeptide, or its fragment or a

cell comprising the polypeptide or its fragment with the compound, and
CC determining the chemical/phenotypic effect of the compound upon the cell.
CC Also disclosed are methods for modulating lymphocyte activation or
CC migration in a subject, by administering to the subject a therapeutically
CC effective amount of an identified compound, an EDG polypeptide or a
CC nucleic acid encoding an EDG, or its fragment, and for screening for
CC modulators of lymphocyte activation, by transfecting into lymphocytes a
CC cDNA library, stimulating T or B cell receptors of the lymphocytes,
CC screening for modulation of lymphocyte activation by detecting the level
CC of CD69 cell surface expression and rescuing cDNAs that modulate
CC lymphocyte activation. The method is useful for identifying a compound
CC (such as an antibody, antisense molecule, small organic molecule,
CC sphingolipid or a sphingolipid analogue) that modulates lymphocyte
CC activation or migration. The compounds identified are useful for the
CC treatment (e.g. gene therapy) of diseases such as asthma, allergy,
CC autoimmune diseases such as multiple sclerosis, scleroderma, pernicious
CC anaemia, insulin-dependent diabetes mellitus, conditions related to organ
CC and tissue transplant such as graft-versus-host disease, acute and
CC chronic inflammation, an infection such as viral, fungal, protozoal or
CC bacterial infections and diseases in which activation of immune response
CC and stimulation of lymphocyte migration is desired. The sequence
CC presented is the human EDG-5 protein
XX
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 6; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
DB 1 MGSLEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIWVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCGLHLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRRSHADMAAPQTALLKTVTVILG 240
DB 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRRSHADMAAPQTALLKTVTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTPFLGNTVV 353
DB 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLERGMHMTPTPFLGNTVV 353

RESULT 8
ABP82010
ID ABP82010 standard; protein; 353 AA.
XX ABP82010;
XX 04-MAR-2003 (first entry)
XX Human sphingolipid receptor Edg5 protein SEQ ID NO:508.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regenerative-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
FN WO2002061087-A2.
XX
PD 08-AUG-2002.
XX
XX 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burner GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
DR N-PSDB; ABZ42860.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 6; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVLCCAIWENLLVLIIVAR 60
DB 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVLCCAIWENLLVLIIVAR 60

QY 61 NSKFSHMYLFLGNLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120
DB 61 NSKFSHMYLFLGNLAASDLGAVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120

QY 121 FSLIAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSIVLGGPIILGNWCLGLEACS 180
DB 121 FSLIAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSIVLGGPIILGNWCLGLEACS 180

QY 181 TVLFLYAKHYVLCVVTTFISILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240
DB 181 TVLFLYAKHYVLCVVTTFISILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240

DB 181 TVLFLYAKHYVLCVVTTFISILLAVVALYVRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240
QY 241 VFIVCWLPAPFSIILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAPFSIILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPVGVGQRRRGTPGHHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353
DB 301 RPLQWRPVGVGQRRRGTPGHHLLPLRSSSSSLERGMHMTPTPTFLEGNTVV 353

RESULT 9
ADC40485
ID ADC40485 standard; protein; 353 AA.
XX
AC ADC40485;
XX
DT 18-DEC-2003 (first entry)
XX
DE Protein of human EDG-5.
XX
KW gene expression analysis; collective quantitative analysis;
KW G protein coupled receptor; tyrosine oxidase receptor family;
KW ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis;
KW myocardial infarction; infarct; ischaemic disease; GPCR; human; EDG-5.
OS Homo sapiens.
XX
XX WO2003052096-A1.
XX
PD 26-JUN-2003.
XX
PF 13-DEC-2002; 2002WO-JP013097.
XX
PR 14-DEC-2001; 2001JP-00382053.
PR 21-FEB-2002; 2002JP-00045104.
PR 15-MAY-2002; 2002JP-00140111.
PR 18-NOV-2002; 2002JP-00333769.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Hinuma S, Kobayashi M, Arai T, Fukusumi S, Fujii R, Komatsu H;
PI Matsumura F, Kawamata Y, Ogi K;
XX
XX WPI; 2003-533023/50.
DR N-PSDB; ADC40486.
XX
XX Method for gene expression analysis for treatment of cancers.
XX
XX Disclosure; SEQ ID NO 46; 261pp; Japanese.
XX
XX The invention relates to a novel method for gene expression analysis by
CC collective quantitative analysis of the expression of a number of genes
CC to identify those that are promoted or inhibited in a given cell or
CC tissue. The genes are preferably gene families such as the G protein
CC coupled receptor family, tyrosine oxidase receptor family, or ion channel
CC gene family. The methods may be used in treatment of cancers, including
CC prostate, ovarian, stomach, bladder, breast, and cancer of the
CC intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used
CC in the treatment and prevention of atherosclerosis, myocardial
CC infarction, infarct or ischaemic disease of the brain. This sequence
CC represents a protein of human EDG-5 of the invention.
XX
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 7; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVLCCAIWENLLVLIIVAR 60
DB 1 MGSLSYSLNPNKQVQEHYNTKETLETQTTTSROVASAFIVLCCAIWENLLVLIIVAR 60

QY 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSATILSASV 120
 Db NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSATILSASV 120
 QY 121 FSLLAIAIRHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPILGWNCIGHLEACS 180
 Db 121 FSLLAIAIRHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPILGWNCIGHLEACS 180
 QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTIVIG 240
 Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTIVIG 240
 QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSLERGMHMTPTFLEGNTVV 353
 Db 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSLERGMHMTPTFLEGNTVV 353

RESULT 10
 ADD11247
 ID ADD11247 standard; protein; 353 AA.
 XX
 AC ADD11247;
 DT 01-JAN-2004 (first entry)
 XX
 DE Human EDG5 protein SEQ ID NO:3.
 XX
 KW Type II diabetes mellitus; venous thrombosis; pulmonary embolism; EDG5;
 KW EDG5 V286A; antidiabetic; thrombolytic; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003085130-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 07-APR-2003; 2003WO-BP003569.
 XX
 PR 09-APR-2002; 2002EP-00007879.
 XX
 PA (AVET) AVENTIS PHARMA DEUT GMBH.
 XX
 PI Kozian D, Kostenis E, Siegler K, Jacobs M, Deleuze J, Ricard S;
 PI Mace S;
 DR WPI; 2003-804314/75.
 DR N-PSDB; ADD11248.
 XX
 PT Identifying an increase in risk for Type II diabetes mellitus and/or
 PT venous thrombosis/pulmonary embolism comprises determining in a probe the
 PT presence of amino acid exchange at position 286 from Val to Ala in the
 PT EDG5 protein.
 XX

Example 2; SEQ ID NO 3; 21pp; English.
 XX
 CC The present invention describes a method for identifying an increase in
 CC risk for Type II diabetes mellitus and/or venous thrombosis/pulmonary
 CC embolism, comprising determining the presence of amino acid exchange at
 CC position 286 from Val to Ala in the EDG5 protein. Also described: (1) a
 CC method for screening pharmaceuticals useful for treating and/or
 CC preventing type II diabetes and/or venous thrombosis/pulmonary embolism,
 CC where a cell or cell extract is used that contains EDG5 with the amino
 CC acid exchange, or the variation in the nucleotide sequence of EDG5
 CC protein or the EDG5-286-AA; (2) a method for adapting the dosage of the
 CC pharmaceutical described above by testing the human cell for the presence
 CC of EDG5 with the amino acid exchange, or the variation in the nucleotide
 CC sequence of EDG5 protein or the EDG5-286-AA; (3) a method of selecting
 CC patients who will respond type II diabetes and/or venous
 CC thrombosis/pulmonary embolism by testing the probe of the respective

CC patient for the presence of EDG5 with the amino acid exchange, or the
 CC variation in the nucleotide sequence of EDG5 protein or the EDG5-286-AA;
 CC and (4) a test kit for testing the presence of the amino acid exchange,
 CC or the variation in the nucleotide sequence of EDG5 protein or the EDG5-
 CC 286-AA. EDG5 has antidiabetic and thrombolytic activities, and can be
 CC used in gene therapy. The methods are useful for identifying an increase
 CC in risk for type II diabetes mellitus and/or thrombosis/pulmonary
 CC embolism, and for screening pharmaceuticals useful for treating type II
 CC diabetes mellitus and/or venous thrombosis/pulmonary embolism. The
 CC methods are also useful for adapting the dosage of a pharmaceutical
 CC useful for treating the above diseases. The methods are useful for
 CC selecting patients who will respond to the pharmaceutical. The present
 CC sequence represents the human EDG5 protein, which is used in an example
 CC from the present invention.

SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 7; Length 353;
 Best Local Similarity 98.9%; Pred. NO. 9.3e-175;
 Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKQOEHYNTKETLETTSTROVASAFIVILCCAIIVVENLLVIAVAR 60
 Db 1 MGSLYSEYLNPNKQOEHYNTKETLETTSTROVASAFIVILCCAIIVVENLLVIAVAR 60
 QY 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSATILSASV 120
 Db 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSATILSASV 120
 QY 121 FSLLAIAIRHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPILGWNCIGHLEACS 180
 Db 121 FSLLAIAIRHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPILGWNCIGHLEACS 180
 QY 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTIVIG 240
 Db 181 TVPLYAKHYVLCVVTIFSIILLAVVALVRYICVVRSSHADMAAPQTALLKTTIVIG 240
 QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLNPVIYTWRSRDLRREVL 300
 QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSLERGMHMTPTFLEGNTVV 353
 Db 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSLERGMHMTPTFLEGNTVV 353

RESULT 11
 ADD90760
 ID ADD90760 standard; protein; 353 AA.
 XX
 AC ADD90760;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Edg5 receptor.
 XX

KW receptor; human; Edg5 receptor; gastrointestinal disorder;
 KW cardiovascular disorder; hypertension; diabetes; respiratory disorder;
 KW asthma; immune disorder; cognitive disorder; memory disorder; obesity;
 KW pain; psychotic behaviour; affective disorder; migraine; cancer; AIDS;
 KW wound healing; ischaemia-reperfusion injury-related disease.

OS Homo sapiens.
 XX
 XX US2003130493-A1.
 PN
 PD 10-JUL-2003.
 XX
 XX 26-AUG-2002; 2002US-00228762.
 PF
 XX 22-FEB-1999; 99US-00253998.
 PR
 PR 16-JUL-1999; 99US-00356315.
 XX

PA (BONI/) BONINI J A.
PA (HUAN/) HUANG L Y.
PA (BORO/) BOROWSKY B E.
PA (SALO/) SALON J A.
PA (WILS/) WILSON A.
PA (NAGO/) NAGORNY R.
XX
XX
XX Bonini JA, Huang LY, Borowsky BE, Salon JA, Wilson A, Nagorny R;
XX WPI; 2003-829581/77.
XX
XX New mammalian Edg7 receptor proteins and nucleic acids encoding mammalian
PT Edg7 receptors, useful for diagnosing and treating an abnormality
PT associated with the activity of the mammalian Edg7 receptor, e.g. asthma,
PT migraine or cancer.
XX
XX Disclosure; SEQ ID NO 19; 64pp; English.
PS
XX The invention relates to an isolated nucleic acid encoding a mammalian
CC Edg7 receptor. The mammalian Edg7 receptor proteins and nucleic acid
CC encoding the proteins are useful for diagnosing and treating an
CC abnormality associated with the activity of the mammalian Edg7 receptors,
CC e.g. gastrointestinal disorder, a cardiovascular disorder, hypertension,
CC diabetes, respiratory disorder, asthma, immune disorder, cognitive
CC disorder, memory disorder, obesity, pain, psychotic behaviour, affective
CC disorder, migraine, cancer, AIDS, wound healing, or ischaemia-reperfusion
CC injury-related diseases. The nucleic acids and proteins are also useful
CC for developing and designing drugs with higher specificity and fewer side
CC effects. The nucleic acid probes are useful for detecting nucleic acid
CC encoding mammalian Edg7 receptors and antisense oligonucleotides
CC complementary to the nucleic acid sequences. The methods are also useful
CC for identifying agonists and antagonists of Edg7 receptors. The present
CC sequence represents the amino acid sequence of the human Edg5 receptor.
XX
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 7; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKQVQEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
Db 1 MGSLSYELNPNKQVQEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVLGGLPILGNWCLGHLRACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVLGGLPILGNWCLGHLRACS 180

QY 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALLKTTVILG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALLKTTVILG 240

QY 241 VFVLCWLPAFSILLDDYACPVHSCPILYKAYHLYFAVSTLNSLLNPVIYTWRSRLRRLV 300
Db 241 VFVLCWLPAFSILLDDYACPVHSCPILYKAYHLYFAVSTLNSLLNPVIYTWRSRLRRLV 300

QY 301 RPLQWRPQVGQVGRGRTGCHHLLPLRSSSSSLRGMHMTPTSFLEGNTV 353
Db 301 RPLQWRPQVGQVGRGRTGCHHLLPLRSSSSSLRGMHMTPTSFLEGNTV 353

RESULT 12
ID ADH57161
XX ADH57161 standard; protein; 353 AA.
XX
XX ADH57161;
XX
DT 25-MAR-2004 (first entry)
XX

DE Human endothelial differentiation factor 5 (EDG5) protein SeqID 3.
XX
KW G protein coupled receptor; EDG5; type II diabetes mellitus;
KW venous thrombosis; pulmonary embolism; endothelial differentiation gene;
KW EDG.
XX
OS Homo sapiens.
XX
XX US2003219808-A1.
XX
XX 27-NOV-2003.
XX
XX 21-MAR-2003; 2003US-00393870.
XX
XX 09-AUG-2002; 2002US-0402305P.
XX
XX (KOZI/) KOZIAN D.
XX (KOST/) KOSTENIS E.
XX (SIEG/) SIEGLER K.
XX (JACO/) JACOBS M.
XX (DELE/) DELEUZE J.
XX (RICA/) RICARD S.
XX (MACE/) MACE S.
XX
XX Kozian D, Kostenis E, Sieglér K, Jacobs M, Deleuze J, Ricard S;
XX Mace S;
XX
XX WPI; 2004-060183/06.
XX N-PSDB; ADH57162.
XX
XX Identifying an increase in risk for type II diabetes mellitus, venous
PT thrombosis, pulmonary embolism or its combination in subject by
PT determining whether amino acid residue at position 286 of EDG5 protein is
PT alanine.
XX
XX Example 2.4; SEQ ID NO 3; 10pp; English.
PS
XX This invention relates to a novel method for identifying an increase in
CC risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism
CC or a combination thereof. Specifically, it refers to a the endothelial
CC differentiation gene 5 (EDG5) located on chromosome 19p13.2, which
CC encodes a G protein coupled receptor protein. The present invention
CC describes an immunochemically reactive labelled antibody based kit that
CC can be used to identify the Val286Ala variation in the EDG5 protein
CC encoded by a single nucleotide polymorphism. Furthermore, this allele
CC encoding the V286A variant represents a genetic marker that can be useful
CC for preventative treatments of the aforementioned diseases, as well as
CC for adapting drug dosage for patients, for drug screening purposes or for
CC patient selection in phase or clinical studies. This polypeptide sequence
CC is the human EDG5 protein of the invention.
XX
SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 8; Length 353;
Best Local Similarity 98.9%; Pred. No. 9.3e-175;
Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKQVQEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
Db 1 MGSLSYELNPNKQVQEHYNYTKETLETQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVLGGLPILGNWCLGHLRACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVLGGLPILGNWCLGHLRACS 180

QY 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALLKTTVILG 240
Db 181 TVLPYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSRSHADMAAPQTLALLKTTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 QY 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNVTW 353
 DB 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNVTW 353

RESULT 13

ADJ62652
 ID ADJ62652 standard; protein; 353 AA.

XX AC ADJ62652;

XX DT 06-MAY-2004 (first entry)

XX DE Human endothelial differentiation gene 5 protein.

XX KW Human; receptor; antisense gene therapy;
 KW endothelial differentiation gene 5; EDG5; G protein-coupled receptor;
 KW development; wound healing; tissue regeneration; cellular proliferation;
 KW apoptosis; cancer; angiogenesis; inflammation;
 KW hyperproliferative disorder; developmental disorder.

XX OS Homo sapiens.

XX PN US2004029274-A1.

XX PD 12-FEB-2004.

XX PF 09-AUG-2002; 2002US-00215821.

XX PR 09-AUG-2002; 2002US-00215821.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Wyatt J;

XX DR WPI; 2004-179674/17.

XX DR N-PSDB; ADJ62544.

XX PT New antisense oligonucleotide targeted to nucleic acid encoding
 PT endothelial differentiation sphingolipid G-protein-coupled receptor 5,
 PT for treating cancer, developmental disorder or a condition arising from
 PT aberrant apoptosis.

XX PS Disclosure; Page 31-32; 50pp; English.

XX CC The invention relates to a compound 8-80 nucleobases in length targeted
 CC to, and which specifically hybridises with a nucleic acid molecule
 CC encoding endothelial differentiation gene 5 (EDG5), a G protein coupled
 CC receptor, involved in development, wound healing, tissue regeneration,
 CC cellular proliferation, apoptosis, cancer, angiogenesis and
 CC inflammation), and inhibits the expression of EDG5, i.e. is an antisense
 CC (AS) oligonucleotide. Also included are a composition comprising the
 CC compound and a carrier or diluent and a method for screening an antisense
 CC compound (by contacting a preferred target region of a nucleic acid
 CC molecule encoding EDG5 with one or more candidate antisense compounds
 CC comprising at least an 8-nucleobase portion that is complementary to the
 CC preferred target region and selecting for one or more candidate antisense
 CC compounds that inhibit the expression of a nucleic acid encoding EDG5).
 CC The compound, composition and methods are useful for treating a disease
 CC or condition associated with EDG5, such as a hyperproliferative disorder,
 CC developmental disorder or a disease or condition arising from aberrant
 CC apoptosis. They are also useful in research and diagnostics for
 CC modulating the expression of EDG5. Experimental protocols are described
 CC but no results are given. The present sequence is the human EDG5 protein.

XX SQ Sequence 353 AA;

Query Match 98.8%; Score 1787; DB 8; Length 353;

Best Local Similarity 98.9%; Pred. No. 9.3e-175;

Matches 349; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MGSLSYELNPNKVOEHYNYTKETLETQTTTSRQVASAFIVILCCAIVVENLLVLAVAR 60
 DB 1 MGSLSYELNPNKVOEHYNYTKETLETQTTTSRQVASAFIVILCCAIVVENLLVLAVAR 60
 QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
 DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
 QY 121 FSLAIAIAERHVAIAKVKLYGDKSCRMILLIGASKWLSLVLGGLPILGNCLHLEACS 180
 DB 121 FSLAIAIAERHVAIAKVKLYGDKSCRMILLIGASKWLSLVLGGLPILGNCLHLEACS 180
 QY 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKKTIVILG 240
 DB 181 TVLPLYAKHYVLCVVTIFSIILLAVVALYVRIYCVVRSSHADMAAPQTLALKKTIVILG 240
 QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 QY 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNVTW 353
 DB 301 RPLQCRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNVTW 353

RESULT 14

ADO29293
 ID ADO29293 standard; protein; 353 AA.

XX AC ADO29293;

XX DT 29-JUL-2004 (first entry)

XX DE Human GPCR EDG5, SEQ ID NO:394.

XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.

XX OS Homo sapiens.

XX PN WO2004040000-A2.

XX PD 13-MAY-2004.

XX PF 09-SEP-2003; 2003WO-US028226.

XX PR 09-SEP-2002; 2002US-0409303P.

XX PR 09-APR-2003; 2003US-0461329P.

XX PA (PRIM-) PRIMAL INC.

XX PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX PI Madisen L, Meilwain XL, Pavlova MN, Vassilatis D, Zeng H;

XX DR WPI; 2004-390329/36.

XX DR N-PSDB; ADO29865.

XX PT Novel mammalian G protein coupled receptors, useful for identifying

CC Chronic obstructive pulmonary disease. The nucleotide sequences encoding
CC EDG5 are useful as hybridization probes, in constructing oligomers for
CC PCR, for chromosome and gene mapping, in the recombinant production of
CC EDG5, in generating antisense DNA or RNA and in molecular biology
CC techniques that have not yet been developed. EDG5 polypeptides are useful
CC for immunising a mammal to produce polyclonal antibodies and for
CC diagnostic purposes. This sequence represents the human EDG5 receptor
CC protein of the invention.
XX
XX
SQ Sequence 353 AA;

Query Match	98.8%;	Score 1787;	DB 8;	Length 353;
Best Local Similarity	98.9%;	Pred. No. 9.3e-175;		
Matches 349;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;

QY	1	MGSLYSEYLNPNKVKQEHYNYTKETLETOETTSRQVASAFIVILCCAIVVVENLLVLIAR	60
DB	1	MGSLYSEYLNPNKVKQEHYNYTKETLETOETTSRQVASAFIVILCCAIVVVENLLVLIAR	60
QY	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAFITLSASV	120
DB	61	NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAFITLSASV	120
QY	121	FSLLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLIISLVLGGLPILGNCLGLEACS	180
DB	121	FSLLATAIERHVAIAKVKLYGSDKSCRMILLIGASWLIISLVLGGLPILGNCLGLEACS	180
QY	181	TVLPLYAKHYVLCVVTIFSIILLAVVALVRIYCVVRSSHADMAAPQTALLKTTVILG	240
DB	181	TVLPLYAKHYVLCVVTIFSIILLAVVALVRIYCVVRSSHADMAAPQTALLKTTVILG	240
QY	241	VFTVCWLPAPFILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL	300
DB	241	VFTVCWLPAPFILLDDYACPVHSCPILYKAHYLFAVSTLNSLLNPVIYTWRSRDLRREVL	300
QY	301	RPLQCRPGVGVGQRRRGTPGHHLLPLRSSSSSLERGMHPTSPTFLEGNTVV	353
DB	301	RPLQCRPGVGVGQRRRGTPGHHLLPLRSSSSSLERGMHPTSPTFLEGNTVV	353

Search completed: December 4, 2005, 06:46:54
Job time : 131 secs

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; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-8

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Query Match	12.4%;	Score	224.5;	DB	6;	Length	430;
Best Local Similarity	24.3%;	Pred. No.	2.6e-12;				
Matches	99;	Conservative	59;	Mismatches	128;	Indels	121;
Gaps	17;						
QY	35	VASAFVILCCATWENLVLIAVARNSKPHSAMYFLGNLAASDLLAGVAFVANTLLSG	94				
DB	48	VAYALIFLLC--WVGNTLVCFVLKRNHHTVNNPILNLAVSDLLGVFCMFTTLVDN	104				
QY	95	SVTLRLTPQWFAREGSAF-----ITLSASVFSLLAIAIER-----HVAIAK	136				
DB	105	LIT-----GWPFDNATCKMSGLVQGMSSVASVETLVAIAVERFCIVHPFREK	152				
QY	137	VKLYGSDKSCRMILLIGASWLISLVL--GGFLPILGNCLGH--LEACSTVLPVLYAKHYV	191				
DB	153	LTUR-----KALVTAVIWAALLMCPBSAVITLVTREHHFMDARNRSYPLYS	202				
QY	192	LC-----VVTIFSIIILAIVALYVRIYCVVR-----SSHADMAA	225				
DB	203	CWEANPEKGMRRVYTVTFSHIYLAFLALIVVMYARIARKLQCAPGAPGGEAAADPA	261				
QY	226	PQTALLKTVTVVLGVFI-VCWLPAPRSILL-LDY---ACPVHSCPILYKAHYXFAVSTLN	280				
DB	262	SRRARVWHMLNVVALFFFTLSWLPMLALLLLIDYGQLSAPQLHLVTYVYFAFWLPAFN	321				
QY	281	SLANPVITYWRSRLRR---EVLRLPQCWRP-----	308				
DB	322	SSANPIIYGFENFRGFOAAFRALCPFPSGSHKEAYSERPGGLLHRRVYVVVRPSDS	381				
QY	309	GVGVQVRRRGTTGGHLLPLURSSSSLERGM-----HMP-TSPTTF	346				
DB	382	GLPSESGPSSGAPRGRLPLNRNGVAHGLPREGPGCSHLPLATIPAW	428				

```

RESULT 6
US-10-992-577-2
; Sequence 2, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-2

```


QY 251 SILL-DYA-CPVHSCPIYKAHYFA--VSTLSILNPVVIYTWRSRLR 297
Db 394 TLWMLSDYADLSPNELQIINIIYIPFAHWLAFGNSVNIYGFNFR 444

RESULT 9

US-10-992-577-44
; Sequence 44, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Bayer HealthCare AG
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Human 5HT6 Receptor
; FILE REFERENCE: LeA 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-502-893-2

Query Match 11.0%; Score 199.5; DB 6; Length 417;
Best Local Similarity 22.7%; Pred. No. 3.2e-10;
Matches 88; Conservative 74; Mismatches 123; Indels 103; Gaps 17;
QY 20 YTKETLETQBTTSROVASAFIVLCCAIIVVENLLVIAVARNSKFSAMYLFLGNLAASD 79
Db 34 YMYYLHQHVTHAVFISSYFLFFLC--WGVTVVCFVIRNRYMHTVTFIFNLASD 91
QY 80 LLAGVAFVANTLS-----GSVTLRLTPVQWFAREGSFITTLSASVFSLLAIAIERH 131
Db 92 LLVGIFCMPITLLDNIAGWPFGSSMCKISGLV---QG---ISVAASVFTLVAIAVDRF 144
QY 132 VAIA---KVKLYGSDSKRCMLLIGASWLSLVLGGLPIL----- 168
Db 145 RCVVYFPFKP-----LTVKTAFAVMIVIIINGLAITIMTPSAIMLHVQEEKYRVR 193
QY 169 --GWNCLGHLEAGSTVPLKAYHYVLCVWTIFSIILLAIYALVYVRYCVVRS----- 219
Db 194 LSHNKTSIVYWCREDWQEMRIYTV-LFATIVLPLSLIVIMYRIGASLFKTSAH 252
QY 220 -----HADMAAPQTLALAKTVTVILGVFVCMWLPAPFSLILL-DYA-CPVHSCPI 267
Db 253 STGKQRLQEWHSKKQKVKMLLTVAL--LFILSLPLWTLMLLSYADLSPNKLVI 309
QY 268 YKAHYFA--VSTLSILNPVVIYTWRSRLR-----REVLPLOCWRPGVGVQGR 315
Db 310 NIIVYFPAHWLAFNCNSVNIYGFNFRSGFDQFQCKKVKQEAY-----GLRAK 365
QY 316 RRGGTPGHLLPLRSSSSSLRGMHMTS 343
Db 366 RN-----LDINTSGLL---VHEPAS 382

RESULT 10

US-10-502-893-2
; Sequence 2, Application US/10502893

; Publication No. US20050255529A1
; GENERAL INFORMATION:
; APPLICANT: Bayer HealthCare AG
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Human 5HT6 Receptor
; FILE REFERENCE: LeA 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-502-893-2

Query Match 10.9%; Score 196; DB 6; Length 440;
Best Local Similarity 25.5%; Pred. No. 6.7e-10;
Matches 96; Conservative 51; Mismatches 135; Indels 94; Gaps 17;
QY 35 VASAFIVILCCAIIVVENLLVLI-----AVARNKFSAMYLFLGNLAASDLLAGVAF--- 86
Db 29 VAAALCVVIALTAANAANSLIALICTQPALRNTSNF-----PLVSLFTSDLMVGLVVMPP 82
QY 87 -VANTLLSGSVTLRLTPVQWFAREGSFITTLSASVFSLLAIAIERHVAIAVKLYGSDKS 145
Db 83 AMNLALYGRWVLARGCLLWTAFD---VMCCSASINCLISLDYLLLSPLRYKLRWT 139
QY 146 -CRMILLIGASWLSLVLGGLP-ILGWNCLGHLE-----ACSTVLPLKAYHYVLCVVTI- 197
Db 140 PLRALALVIGAWSLAALASFLPLLGHGHELGHARPVPQCRLASL---PFVLVASGLT 196
QY 198 FSIIILLAIYALVYVRYCVVRSADMA-----AQTLAL----- 231
Db 197 FFLPSGAICTFYCRILLAAKQAVQVSLTTGMSQASSETLQVPRTPRGVSASRRRLA 256
QY 232 -----LK---TVTVILGVFVCMWLPAPFSLILLDYACPVHSCPIYKAYHYFAVST--- 278
Db 257 TKHSRKALKASUTLGLGMFFVTLPEFVANIIVQAVDCIS-PGL-----FDVLTWLG 309
QY 279 -LNSLLNPVIYTWRSRLRREVLRLPQCWR-----PGVGVQGRRRGGTGGHLLPL 328
Db 310 YCNSTMNPIIYFLWRFKRALGRFLPCPCPRQASLASPSLRTSHSGPRPG----- 363
QY 329 RSSSSSLRGMHMTSP 344
Db 364 ---LSLQVLPPLPP 376

RESULT 11
US-10-980-388-118
; Sequence 118, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325-US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02

```
; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-067-884-8

Query Match      10.2%; Score 184; DB 7; Length 419;
Best Local Similarity 25.5%; Pred. No. 6.5e-09;
Matches 92; Conservative 49; Mismatches 132; Indels 88; Gaps 17;

Qy 37 SAFIVILCCAIVVENLVLIAVARNSKFHSAMYLFLGNLAASDLLAGV---AFVANTLLS 93
Db 85 SAIMIFILFVSFLGNLVCLMVYQKAAMRSAINILLASLAFADMLLAVLNPPFALVTIL- 143
Qy 94 GSVTLRLTPVQWFAREGSAPITLSA--SVFSLLAIAIERHVAIA---KVKLYGSDKSCR 147
Db 144 ---TTRWIFGKFCRVSMFFWLFVIEGVAILLIISIDRFLIIVQRQDKLNPY-----R 194
Qy 148 MLLIGASWLIS-----LVLGG----LPILGNWCL-GHLEACSTVLPLVAKHYVLCVVT 196
Db 195 AKVLIAVSWATSCFVAPPLAVGNPDQLQPSRAPQCVFGY-----TTNPGYQAYVILISLI 249
Qy 197 IFSILLIAIV-----ALYRIY-----CVVRSSHADMAAPQ-----T 228
Db 250 SFFPFLVILVSEFMGIINTLRHNAIRHISYPEGICLSQASKGLMSLQRPQMSIDMGFK 309
Qy 229 LALLKTTVILGVFIVCWLPAFSTILLDYACPVHSCFPLVKAHYKFAVST-----LNS 281
Db 310 TRAFFTLLIFAFVIVCWAP-FTYISLVATFSKH---FYQHNFIFEISITWLLWLCVLKS 364
Qy 282 LLNPVIYTWRSR---DLRREVLRLPQCWRPGVQVGRRRGTGPHHLLPLRSSSSLSBERGM 338
Db 365 ALNPLIYYWRIKPKHDAACLDMPKSKFKLPQL-----PGHTRRRIRPSAVVYVCGE 414
Qy 339 H 339
Db 415 H 415

RESULT 13
US-10-980-388-112
; Sequence 112, Application US/10980388
; Publication No. US2005025490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325-US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
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; FILE REFERENCE: 20609/305
; CURRENT APPLICATION NUMBER: US/11/067,884
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/190,370
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 09/811,838
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-067-884-8

Query Match      10.2%; Score 184; DB 6; Length 342;
Best Local Similarity 22.4%; Pred. No. 5.2e-09;
Matches 64; Conservative 53; Mismatches 103; Indels 56; Gaps 11;

Qy 48 VVENLLVLIIVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTFVQWFA 107
Db 46 VFGNLLVMTSVLHFQKLSHPTNFIASLACADFLVGVTVMLFSM-----VRTVESCWYF 99
Qy 108 REGSAFITLS-----ASVFSLLAIAIERHVAIAKVKLYGSDKSCRM-LILIGASWL 157
Db 100 --GAKFCTTHSCCDVAFCYSSVLLHCFICIDRIYIVTVDPLVYATKFTVSVSGICISVSI 157
Qy 158 ISLVGLGLP-----ILGNWCLGHLEACSTVLPLVAKHYVLCVVTIFSIIILA 204
Db 158 LPLTYSAGVFTGVNDDGLELVSALNCVG---GCQIV---SQGWLIDFLFIPTLV 211
Qy 205 IVALYVRIYCVVR-----SSHADMAAPOTLALLKTTVITVLGVFIVCWL 247
Db 212 MIIYSKIFLIAKQQAIIETTSSKVESSESYKIRVAKRERKAAKTLGVTVLAFVISWL 271
Qy 248 PAFSTILLD-----YACPVHSCFI-LYKAHYFPAVSTLNSLNPVIY 288
Db 272 FYTVDILIDAFMGFLTPAYIIEICWSAY-----NSAMNPLIY 310

RESULT 12
US-11-067-884-8
; Sequence 8, Application US/11067884
; Publication No. US20050261252A1
; GENERAL INFORMATION:
; APPLICANT: Tigyi, Gabor
; APPLICANT: Dailon, James T.
; APPLICANT: Sardar, Vineet M.
; APPLICANT: Elrod, Don B.
; APPLICANT: Xu, Huiping
; APPLICANT: Baker, Daniel L.
; APPLICANT: Wang, Dean
; APPLICANT: Lilom, Karoly
; APPLICANT: Fischer, David J.
; APPLICANT: Nusser, Nora
; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
; TITLE OF INVENTION: USE
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; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-112

Query Match
Best Local Similarity 9.3%; Score 167.5; DB 6; Length 508;
Matches 49; Conservative 48; Mismatches 84; Indels 17; Gaps 6;

QY 35 VASAFITLCCATWENLVLIAVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLS 94
DB 33 IRSTVLVIFLAASFVGNVIALVLRKPOLQVTRFNFLLVTDLLQ-LSLVAPWVAT 91

QY 95 SVTLRTPVQWFAREG--SAFITLS-----ASVFSLLAIAERHVAIAKVLGYGDKSCR 147
DB 92 SV-----PLFWPLNSHFCTALVSLTHLFAFASVNTIVVSDRYLSIIHPLSYPSQWQR 146

QY 148 M-LLLIGASLWLSLGGIPILGNCLGHLE---ACSTVLPLYAKHYVLCVVTIPSILL 203
DB 147 RGVLLYGTWIVAILQSTPPLYGWAQAFDERNALCSMIWGASPSYTLISWFSVFIPLI 206

QY 204 AIVALVRIYCVVRSSHA 221
DB 207 VMIACSVVFCARQHA 224

RESULT 14
US-10-627-633-2
; Sequence 2, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brennand, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-633-2

Query Match
Best Local Similarity 7.8%; Score 141; DB 6; Length 415;
Matches 87; Conservative 54; Mismatches 128; Indels 86; Gaps 20;

QY 4 LYSEYL-----NPNKVQEHYNTKETLETQSTTSRQVASAFITLCCATWENLVL 54
DB 35 LPSQYLMELSEHSWNSQTDLHY-----VLKPGEVAT---ASIFFGILWLWPSIFGNSLV 86

QY 55 LIAVARNKSFHSAMYLFLGNLAASDLLAGVAFVANTLLS-----GSVTLRLLTPVQWF 106
DB 87 CLVIHRSRRTOSTTNYFVVSMA CADLLISVASTPPVLLQFTTGRWTLGSATCKV--VRYF 144

QY 107 AREGSAFITLSASFVSLAIAERHVAIA-----KVLGYGDKSCRMILLIGASWLI--S 159
DB 145 -----QYLTPGVQIYVLLSICIDRFYTIYVPLSPKVSREKAKK-----MIAASWIFDAG 193

QY 160 LVLGGPLILGNCLGHLEACSTVLPL-----LYAKHYVLCVVTIPSILLAI---VALYV 210
DB 194 FVTPVLFYFGSNWDSH---CNFLPSSWEGTAYTVIHFLVGVFVSVLLILFYQVKIKYI 250

QY 211 -RIYCVVRSSHADM-AAPQT-LALLKTVTVILGVFIVCWLPAPFSILL-----DYACPV 261
DB 251 WRIGTDGRTVRRTNVIVPRTKVKTKMFLILNLLFLLSWLP-FHVAQLMHPHEQDYK--- 306

QY 262 HSCPILYKAHYXFA-----VSTLNSLNPVIYTWRSRDLRREV-----LRPQCWR 307
DB 307 -----KSSLVFTAITWISFSSASKPTLYSIYNANFRGRMKETFCMSSMKCYR 354

RESULT 15
US-10-821-234-934
; Sequence 934, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 934
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-934

Query Match
Best Local Similarity 7.8%; Score 140; DB 6; Length 485;
Matches 62; Conservative 59; Mismatches 120; Indels 42; Gaps 11;

QY 51 NELLVIAVARNKSFHSAMYLFLGNLAASDLL--AGVAFVANTLLSGSVTLRLTPVQW-FA 107
DB 180 NIMAIIVFILKMKVKKPAVVMHLATADLVFVSVLPFKISYFSGS-----DMQFG 231

QY 108 REGSAFIT-----LSASFVSLAIAERHVAIAKV-----KLYGDKSCRMILLIGA 154
DB 232 SELCRFVTAAFYCNVMVASILLMTVISIDRF LAVVYPMQSLSWRTLGRASFTCLAIWALAI 291

QY 155 SWLISLVL--GGLPILGNCLGHLEACSTVL-----PLYAKHYVLCVVTIPSILLAI 206
DB 292 AGVVPVLVLEQTIQVPGLN-----ITTCHDVNLNETLEGYYAYFSAFVFPVPIIST 347

QY 207 ALYVRIYCVVRSSHADMAAPQTLALLKTVTVILGVFIVCWLPAPFSILLDDYACPVHSCPI 266
DB 348 VCYSIIRCLSSAVANRSKSRALFLSAA-VFCFIICFGTGNVLLIAHYFLSHT-ST 405

QY 267 LYKAHYXF-----AVSTLNSLNPVIYTWRSRDLRREVLRPLOC 305
DB 406 TEAAVFAVLLCCVSVSISCIDPLIYYASSECQRVYSILCC 448

Search completed: December 4, 2005, 06:42:26
Job time : 7 secs

The Page with (1000)

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:23:06 ; Search time 115.5 Seconds
(without alignments)
1277.002 Million cell updates/sec

Title: US-10-084-507B-17
Perfect score: 1806
Sequence: 1 MGSLSYEVLPNPKVQEHYNY.....LRCGMHPTSPTFLEGNVTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	99.9	353	3	US-09-771-063-2
2	1804	99.9	353	4	US-10-084-507B-17
3	1803	99.8	353	3	US-09-731-030A-19
4	1803	99.8	353	4	US-10-084-507B-22
5	1787	98.9	353	3	US-09-842-316-8
6	1787	98.9	353	3	US-09-971-228-9
7	1787	98.9	353	3	US-09-904-099-33
8	1787	98.9	353	4	US-10-225-567A-508
9	1787	98.9	353	4	US-10-228-762-19
10	1787	98.9	353	4	US-10-393-870-3
11	1787	98.9	353	4	US-10-421-828-8
12	1787	98.9	353	4	US-10-715-117-7
13	1787	98.9	353	5	US-10-498-848-46
14	1783	98.7	353	3	US-09-771-063-4
15	1625.5	90.0	352	4	US-10-084-507B-21
16	1432	79.3	372	3	US-09-904-099-37
17	947	52.4	269	3	US-09-764-886-47
18	947	52.4	269	3	US-09-764-886-47
19	947	52.4	274	3	US-09-764-886-74
20	947	52.4	274	3	US-09-764-891-5338
21	947	52.4	274	3	US-09-764-886-74
22	860.5	47.6	384	3	US-09-904-099-5
23	858.5	47.5	391	3	US-09-904-099-3
24	858	47.5	362	3	US-09-993-844-8
25	854.5	47.3	362	4	US-10-633-438-65
26	854.5	47.3	362	4	US-10-633-438-65
27	854.5	47.3	362	5	US-10-901-772-65

28	854.5	47.3	362	6	US-11-026-435-8	Sequence 8, Appli
29	849	47.0	341	3	US-09-971-228-13	Sequence 13, Appl
30	849	47.0	382	3	US-09-971-228-5	Sequence 5, Appli
31	849	47.0	382	3	US-09-863-455-2	Sequence 2, Appli
32	849	47.0	382	3	US-09-759-514-2	Sequence 1, Appli
33	849	47.0	382	4	US-10-087-192-786	Sequence 237, App
34	849	47.0	382	4	US-10-225-567A-237	Sequence 786, Appl
35	849	47.0	382	4	US-10-295-027-2	Sequence 2, Appli
36	849	47.0	382	4	US-10-429-160-72	Sequence 72, Appli
37	849	47.0	382	4	US-10-211-462-2	Sequence 2, Appli
38	849	47.0	382	5	US-10-491-545A-30	Sequence 30, Appl
39	849	47.0	382	5	US-10-498-848-38	Sequence 38, Appl
40	849	47.0	448	4	US-10-425-114-55760	Sequence 55760, A
41	849	47.0	448	4	US-09-971-228-15	Sequence 15, Appl
42	848	47.0	346	3	US-11-100-593-8	Sequence 8, Appli
43	847	46.9	383	3	US-09-969-711-2	Sequence 2, Appli
44	845	46.8	382	4	US-10-087-192-783	Sequence 783, App
45	845	46.8	382	4	US-10-087-192-783	Sequence 783, App

ALIGNMENTS

RESULT 1

US-09-771-063-2
; Sequence 2, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derek J. Bergsma
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-C1
; CURRENT APPLICATION NUMBER: US/09/771,063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-771-063-2

Query Match 99.9%; Score 1804; DB 3; Length 353;
Best Local Similarity 99.7%; Pred. No. 2.7e-156; Indels 0; Gaps 0;
Matches 352; Conservative 0; Mismatches 1;

QY	1	MGSLSYEVLPNPKVQEHYNYKETTETTSRQVASAFIVILCCAIVVENLLVLI	60
Db	1	MGSLSYEVLPNPKVQEHYNYKETTETTSRQVASAFIVILCCAIVVENLLVLI	60
QY	61	NSKFSHSMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS	120
Db	61	NSKFSHSMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS	120
QY	121	FSLLAIATERHVAIAKVKLYGSKRCRMLLLIGASWLSLVGLPILGMNCLH	180
Db	121	FSLLAIATERHVAIAKVKLYGSKRCRMLLLIGASWLSLVGLPILGMNCLH	180
QY	181	TVLPYAKHYLVCCVTIFSIILLAIVALVRYICVVRSSHADMAAPQTLALK	240
Db	181	TVLPYAKHYLVCCVTIFSIILLAIVALVRYICVVRSSHADMAAPQTLALK	240
QY	241	VFIVCWLPAFSLILLDYACPFVHSCPILYKAHYKFAVSTLNSLLNPVYTW	300
Db	241	VFIVCWLPAFSLILLDYACPFVHSCPILYKAHYKFAVSTLNSLLNPVYTW	300

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QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNTVV 353
Db |||||
301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNTVV 353

RESULT 2
US-10-084-507B-17
; Sequence 17, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084, 507B
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (273)
; OTHER INFORMATION: Leu or Phe
US-10-084-507B-17

Query Match 99.9%; Score 1804; DB 4; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.7e-156;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLSYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVLCCAIIVENLLVLIAR 60
Db |||||
1 MGSLSYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVLCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVLKYGSKCRMLLIGASWLSLVGLGPIIGWNCGLGLEACS 180
Db |||||
121 FSLAIAIERHVAIAKVLKYGSKCRMLLIGASWLSLVGLGPIIGWNCGLGLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTTVILG 240
Db |||||
181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db |||||
241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db |||||
241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300

QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNTVV 353
Db |||||
301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNTVV 353

RESULT 3
US-09-731-030A-19
; Sequence 19, Application US/09731030A
```

```
; Patent No. US20020142375A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: GUPTA, ASHWANI K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

Query Match 99.8%; Score 1803; DB 3; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.4e-156;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLSYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVLCCAIIVENLLVLIAR 60
Db |||||
1 MGSLSYSEYLNPNKVOEHYNYTKETLEQTTSRQVASAFIVLCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db |||||
61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

QY 121 FSLAIAIERHVAIAKVLKYGSKCRMLLIGASWLSLVGLGPIIGWNCGLGLEACS 180
Db |||||
121 FSLAIAIERHVAIAKVLKYGSKCRMLLIGASWLSLVGLGPIIGWNCGLGLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTTVILG 240
Db |||||
181 TVLPLYAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLALLKTTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300
Db |||||
241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300

QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNTVV 353
Db |||||
301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLERGMHMTSPTFLEGNTVV 353

RESULT 4
US-10-084-507B-22
; Sequence 22, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH
; APPLICANT: VIJAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084, 507B
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
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[illegible]

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RESULT 7
US-09-904-099-33
; Sequence 33, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Shankar, Geetha
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-099-33

Query Match      98.9%; Score 1787; DB 3; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240

Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGVQGRRRGTGPHHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQCRPGVGVQGRRRGTGPHHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 8
US-10-225-567A-508
; Sequence 508, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 508
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-508

Query Match      98.9%; Score 1787; DB 3; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYRIYCVVRSSHADMAAPQTLALLKTTVTVLG 240

Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGVQGRRRGTGPHHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQCRPGVGVQGRRRGTGPHHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 9
US-10-228-762-19
; Sequence 19, Application US/10228762
; Publication No. US20030130493A1
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Huang, Ling Yan
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Salton, John A.
; APPLICANT: Wilson, Amy
; APPLICANT: Nagorny, Raisa
; TITLE OF INVENTION: DNA Encoding Edg7 Receptor
; FILE REFERENCE: 58230-a
; CURRENT APPLICATION NUMBER: US/10/228,762
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US/09/356,315
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 09/253,998
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-228-762-19

Query Match      98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKVOEHYNTKETLETQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSISLVGLPLILGNWCLHLEACS 180
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QY 181 TVLPYAKHYVLCVWTIFSIILLAIIVLYVRIYCVVRRSHADMAAPQTLLAKTKTVTVLG 240
DB 181 TVLPYAKHYVLCVWTIFSIILLAIIVLYVRIYCVVRRSHADMAAPQTLLAKTKTVTVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVSCHPILYKAXYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVSCHPILYKAXYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMPSTPTFLEGNVTVV 353
DB 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMPSTPTFLEGNVTVV 353

RESULT 10

US-10-393-870-3
; Sequence 3, Application US/10393870
; Publication No. US20030219808A1
; GENERAL INFORMATION:
; APPLICANT: KOZIAN, Detlef
; APPLICANT: KOSTENIS, Evi
; APPLICANT: SIELGER, Karl-Ernet
; APPLICANT: JACOBS, Martina
; APPLICANT: RICARD, Sylvain
; APPLICANT: MACE, Sandrine
; APPLICANT: DELEUZE, Jean-Francois
; TITLE OF INVENTION: ASSOCIATION OF EDGS POLYMORPHISM WITH TYPE II DIABETES MELLITUS,
; TITLE OF INVENTION: VENOUS THROMBOSIS OR PULMONARY EMBOLISM AND THE USE THEREOF
; FILE REFERENCE: DEAV2002/0019 US NP
; CURRENT APPLICATION NUMBER: US/10/393,870
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-870-3

Query Match 98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASFIVILCCAIIVVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
QY 181 TVLPYAKHYVLCVWTIFSIILLAIIVLYVRIYCVVRRSHADMAAPQTLLAKTKTVTVLG 240
DB 181 TVLPYAKHYVLCVWTIFSIILLAIIVLYVRIYCVVRRSHADMAAPQTLLAKTKTVTVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVSCHPILYKAXYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVSCHPILYKAXYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMPSTPTFLEGNVTVV 353
DB 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMPSTPTFLEGNVTVV 353

RESULT 11

US-10-421-828-8
; Sequence 8, Application US/10421828
; Publication No. US20030219874A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIS, Eva

; APPLICANT: GASENHUBER, Johann
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE
; FILE REFERENCE: 38005-147
; CURRENT APPLICATION NUMBER: US/10/421,828
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: EP 116589.3
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: EP 108858.2
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-421-828-8

Query Match 98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLYSEYLNPNKVOEHYNTKETLETTQTSRQVASFIVILCCAIIVVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLGLEACS 180
QY 181 TVLPYAKHYVLCVWTIFSIILLAIIVLYVRIYCVVRRSHADMAAPQTLLAKTKTVTVLG 240
DB 181 TVLPYAKHYVLCVWTIFSIILLAIIVLYVRIYCVVRRSHADMAAPQTLLAKTKTVTVLG 240
QY 241 VFIVCWLPAFSLILLDYACPVSCHPILYKAXYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVSCHPILYKAXYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMPSTPTFLEGNVTVV 353
DB 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMPSTPTFLEGNVTVV 353

RESULT 12

US-10-715-117-7
; Sequence 7, Application US/10715117
; Publication No. US20040171037A1
; GENERAL INFORMATION:
; APPLICANT: LI, JING
; APPLICANT: POWERS, SCOTT
; APPLICANT: SIN, WUN CHEY
; APPLICANT: YANG, JIANKIN
; TITLE OF INVENTION: AMPLIFIED GENES INVOLVED IN CANCER
; FILE REFERENCE: 38002-0062
; CURRENT APPLICATION NUMBER: US/10/715,117
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: 60/427,202
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/434,434
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-117-7

Query Match 98.9%; Score 1787; DB 4; Length 353;
Best Local Similarity 99.2%; Pred. No. 9.8e-155;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 1 MGSLYSEYLNPNKQOEHNYYTKETLETTQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSLVLGGLPILGNWNLGLHLEACS 180
Db 121 FSLLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSLVLGGLPILGNWNLGLHLEACS 180
Qy 181 TVPLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVWRSSHADMAAPQTLALLKTTVTVLG 240
Db 181 TVPLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVWRSSHADMAAPQTLALLKTTVTVLG 240
Qy 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQCRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMTSPPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMTSPPTFLEGNTVV 353

RESULT 13

US-10-498-848-46
; Sequence 46, Application US/10498848
; Publication No. US20050153289A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Method of Analyzing Gene Expression
; FILE REFERENCE: P02-0155PCT
; CURRENT APPLICATION NUMBER: US/10/498,848
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: JP 2001-382053
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: JP 2002-45104
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: JP 2002-140111
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: JP 2002-333769
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 46
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human
US-10-498-848-46

Query Match 98.9%; Score 1787; DB 5; Length 353;
Best Local Similarity 99.2%; Pred. No. 9,8e-155;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MGSLYSEYLNPNKQOEHNYYTKETLETTQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
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Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSLVLGGLPILGNWNLGLHLEACS 180
Db 121 FSLLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSLVLGGLPILGNWNLGLHLEACS 180
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Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQCRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMTSPPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMTSPPTFLEGNTVV 353
RESULT 14
US-09-771-063-4
; Sequence 4, Application US/09771063
; Patent No. US20010034331A1
; GENERAL INFORMATION:
; APPLICANT: Derek J. Bergsma
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Pamela Lane
; APPLICANT: Xiaotong Li
; APPLICANT: Jeffrey L. Mooney
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: EDG FAMILY GENE, HUMAN H218
; FILE REFERENCE: GP-70431-CI
; CURRENT APPLICATION NUMBER: US/09/771,063
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/150,650
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/082,776
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-771-063-4

Query Match 98.7%; Score 1783; DB 3; Length 353;
Best Local Similarity 98.9%; Pred. No. 2.3e-154;
Matches 349; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1 MGSLYSEYLNPNKQOEHNYYTKETLETTQETTSRQVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATITLSASV 120
Qy 121 FSLLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSLVLGGLPILGNWNLGLHLEACS 180
Db 121 FSLLAIAIERHVAIAKVLKYGSDKSCRMILLIGASWLSLVLGGLPILGNWNLGLHLEACS 180
Qy 181 TVPLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVWRSSHADMAAPQTLALLKTTVTVLG 240
Db 181 TVPLPYAKHYVLCVWTIFSIILLAI VALYVRIYCVWRSSHADMAAPQTLALLKTTVTVLG 240
Qy 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQCRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMTSPPTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGTTGHHLLPLRSSSSSLERGMHMTSPPTFLEGNTVV 353

RESULT 15

US-10-084-507B-21
; Sequence 21, Application US/10084507B
; Publication No. US20030054452A1
; GENERAL INFORMATION:
; APPLICANT: MUNROE, DONALD G.
; APPLICANT: KAMBOJ, RAJENDER
; APPLICANT: PETERS, DIANA
; APPLICANT: KOOSHESH, FATEMEH

```

; APPLICANT: VYAS, TEJAL B.
; APPLICANT: GUPTA, ASHWANI K.
; TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
; FILE REFERENCE: 108074-00023
; CURRENT APPLICATION NUMBER: US/10/084,507B
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-084-507B-21

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Query Match          90.0%; Score 1625.5; DB 4; Length 352;
Best Local Similarity 89.8%; Pred. No. 5.6e-140;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGLYSEYLNPNKVOEHYNYTKETLETOETTSROVASAFIVILCCAIVVENLLVLIAR 60
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DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPQWFAREGSAFILTASV 120

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DB 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLGPLGWNCLHLEACS 180

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DB 181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRYCVVRRSHADMAAPOTLALKTVTVLG 240

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DB 241 VFTVCWLPAPFILLDYPACVHSCPTLYKHYKFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQCWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
DB 301 RPLQCWRPGVGQRRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

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Job time : 117.5 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:10:25 ; Search time 33.5 Seconds
(without alignments)
871.180 Million cell updates/sec

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Perfect score: 1806
Sequence: 1 MGSLEYLNPNKQEHYNY.....LERGMHMTPTFLEGNIVV 353

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1804	99.9	353	2	US-09-582-200A-10
4	1803	99.8	353	2	US-09-582-200A-4
5	1803	99.8	353	2	US-09-582-200A-6
6	1803	99.8	353	2	US-09-582-200A-12
7	1803	99.8	353	2	US-09-731-030A-19
8	1760	97.5	353	2	US-09-274-752D-3
9	1625.5	90.0	352	1	US-08-196-989B-2
10	1625.5	90.0	352	1	US-08-760-936-2
11	1625.5	90.0	352	2	US-09-582-200A-11
12	1625.5	90.0	352	2	US-09-169-205D-24
13	1625.5	90.0	352	2	US-09-225-024-2
14	849	47.0	382	2	US-09-262-477-2
15	847	46.9	383	1	US-08-196-989B-4
16	847	46.9	383	1	US-08-760-936-4
17	847	46.9	383	2	US-09-225-024-4
18	845	46.8	382	2	US-09-542-733-2
19	836.5	46.3	381	1	US-08-845-566-3
20	836.5	46.3	381	1	US-08-467-948A-28
21	836.5	46.3	381	2	US-08-852-824-18
22	836.5	46.3	381	2	US-08-467-947A-28
23	836.5	46.3	381	2	US-09-731-030A-17
24	836.5	46.3	381	4	PCT-US96-10618-18
25	836.5	46.3	381	4	PCT-US96-10618-4
26	831	46.0	382	2	US-09-169-205D-21
27	769	42.6	378	2	US-09-082-088-2

28	769	42.6	378	2	US-09-546-117-2	Sequence 2, Appli
29	769	42.6	378	2	US-09-169-205D-22	Sequence 22, Appl
30	769	42.6	378	2	US-09-731-030A-18	Sequence 18, Appl
31	763	42.2	334	1	US-08-118-270-73	Sequence 73, Appl
32	763	42.2	334	4	PCT-US93-08528-73	Sequence 73, Appl
33	720.5	39.9	500	2	US-09-875-076-30	Sequence 30, Appl
34	533	29.5	384	2	US-09-731-030A-11	Sequence 11, Appl
35	529	29.3	384	2	US-09-731-030A-13	Sequence 13, Appl
36	521	28.8	384	2	US-08-852-824-4	Sequence 4, Appli
37	521	28.8	384	2	US-09-518-383-4	Sequence 4, Appli
38	513	28.4	393	4	PCT-US96-10618-3	Sequence 3, Appli
39	510	28.2	364	2	US-09-169-205D-20	Sequence 20, Appl
40	509	28.2	364	2	US-08-763-938-2	Sequence 2, Appli
41	507	28.1	364	4	PCT-US96-10618-2	Sequence 2, Appli
42	504	27.9	364	2	US-09-731-030A-15	Sequence 15, Appl
43	504	27.9	364	2	US-09-811-838-2	Sequence 2, Appli
44	491	27.2	382	2	US-09-169-205D-23	Sequence 23, Appl
45	491	27.2	382	2	US-09-274-752D-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-582-200A-2
; Sequence 2, Application US/09582200A
; Patent No. 6482609

GENERAL INFORMATION:

; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani

TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE

; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A

; CURRENT FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 09/222,995

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: PCT/CA98/01195

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 60/109,885

; PRIOR FILING DATE: 1998-11-25

; PRIOR APPLICATION NUMBER: 60/080,610

; PRIOR FILING DATE: 1998-04-03

; PRIOR APPLICATION NUMBER: 60/070,185

; PRIOR FILING DATE: 1997-12-30

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (273)..(273)

; OTHER INFORMATION: Unknown Xaa refers to any amino acid

US-09-582-200A-2

Query Match		99.9%;	Score 1804;	DB 2;	Length 353;
Best Local Similarity		100.0%;	Pred. No. 2.6e-146;	Mismatches 0;	Indels 0;
Matches 353;		Conservative 0;			
QY	1	MGSLEYLNPNKQEHYNYTKETLETQETTSRQVASAFIVILCCAI	VVENVLLVIAVAR	60	
Db	1	MGSLEYLNPNKQEHYNYTKETLETQETTSRQVASAFIVILCCAI	VVENVLLVIAVAR	60	
QY	61	NSKPHSAYMLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGS	AFITLSASV	120	
Db	61	NSKPHSAYMLFLGNLAASDLLAGVAVFVANTLLSGSVTLRLTPVQWFAREGS	AFITLSASV	120	
QY	121	FSLLAIAERHVAIAKVKLYGDKSCRMILLIGASWLSISLVLGGLPILGWNCLHLEACS	180		

Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGGPIILGNCLGLEACS 180
Qy 181 TVLPLYAKHYVLCVWTIFSIIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Db 181 TVLPLYAKHYVLCVWTIFSIIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Qy 241 VFIVCWLPAFASILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFASILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 2
US-09-582-200A-5
; Sequence 5, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CONFLICT
; LOCATION: (272)..(274)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: Unknown Xaa = Leu or Pro
US-09-582-200A-5

Query Match 99.9%; Score 1804; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.6e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSLSYSEVLNPNKQVEHNYTKETLETQETTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEVLNPNKQVEHNYTKETLETQETTSROVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTILSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTILSASV 120
Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGGPIILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGGPIILGNCLGLEACS 180

Qy 181 TVLPLYAKHYVLCVWTIFSIIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Db 181 TVLPLYAKHYVLCVWTIFSIIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Qy 241 VFIVCWLPAFASILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFASILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
RESULT 3
US-09-582-200A-10
; Sequence 10, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 polypeptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (273)..(273)
; OTHER INFORMATION: "Xaa" represents any amino acid
US-09-582-200A-10

Query Match 99.9%; Score 1804; DB 2; Length 353;
Best Local Similarity 100.0%; Pred. No. 2.6e-146;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGSLSYSEVLNPNKQVEHNYTKETLETQETTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEVLNPNKQVEHNYTKETLETQETTSROVASAFIVILCCAIWENLLVLIIVAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTILSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTILSASV 120
Qy 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGGPIILGNCLGLEACS 180
Db 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIIGASWLSISLVGGPIILGNCLGLEACS 180
Qy 181 TVLPLYAKHYVLCVWTIFSIIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Db 181 TVLPLYAKHYVLCVWTIFSIIILLAI VALYVRIYCVVRSSHADMAAPQTALLKTKVTIVLG 240
Qy 241 VFIVCWLPAFASILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFASILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGMHMTPTPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGMHMTPTPTFLEGNTVV 353

RESULT 4

US-09-582-200A-4
; Sequence 4, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-200A-4

Query Match 99.8%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYNPNKVOEHYNYTKETLETQTTTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
Db 1 MGSLYSEYNPNKVOEHYNYTKETLETQTTTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLG HLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLG HLEACS 180
QY 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYICVVRSSHADMAAPQTLLKKT VTVILG 240
Db 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYICVVRSSHADMAAPQTLLKKT VTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGMHMTPTPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGMHMTPTPTFLEGNTVV 353

RESULT 5

US-09-582-200A-6
; Sequence 6, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:

; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-582-200A-6

Query Match 99.8%; Score 1803; DB 2; Length 353;

Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLYSEYNPNKVOEHYNYTKETLETQTTTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
Db 1 MGSLYSEYNPNKVOEHYNYTKETLETQTTTSRQVASAFIVILCCAI VVENLLVLI AVAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS AFITLSASV 120
QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLG HLEACS 180
Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGWNCLG HLEACS 180
QY 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYICVVRSSHADMAAPQTLLKKT VTVILG 240
Db 181 TVPLYAKHYVLCVVTFISIIILAVVLYVRYICVVRSSHADMAAPQTLLKKT VTVILG 240
QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGMHMTPTPTFLEGNTVV 353
Db 301 RPLQWRPGVGQRRRGTPGHLLPLRSSSLRGMHMTPTPTFLEGNTVV 353

RESULT 6

US-09-582-200A-12
; Sequence 12, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY R+
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/582,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995

```
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 #36
US-09-582-200A-12

Query Match          99.8%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKVOEHYNYTKETLETTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKVOEHYNYTKETLETTTSROVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLGLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLGLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPFTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPFTFLEGNTVV 353

RESULT 8
US-09-274-752D-3
; Sequence 3, Application US/09274752D
; Patent No. 6812335
; GENERAL INFORMATION:
; APPLICANT: Goetzel, Edward L.
; APPLICANT: An, Songzhu
; TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipide and
; FILE REFERENCE: A-67501/DJB/TAL
; CURRENT APPLICATION NUMBER: US/09/274,752D
; CURRENT FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-274-752D-3

Query Match          97.5%; Score 1760; DB 2; Length 353;
Best Local Similarity 98.3%; Pred. No. 1.5e-142;
Matches 347; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKVOEHYNYTKETLETTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKVOEHYNYTKETLETTTSROVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLGLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLGLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPFTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPFTFLEGNTVV 353

; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: human EDG-4 #36
US-09-582-200A-12

Query Match          99.8%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSLSYSEYLNPNKVOEHYNYTKETLETTTSROVASAFIVILCCAIWENLLVLIIVAR 60
Db 1 MGSLSYSEYLNPNKVOEHYNYTKETLETTTSROVASAFIVILCCAIWENLLVLIIVAR 60

Qy 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLGLEACS 180
Db 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLPLIGWNCGLGLEACS 180

Qy 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240
Db 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSSHADMAAPOTLALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

Qy 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPFTFLEGNTVV 353
Db 301 RPLQCRPGVGQRRRGCTPGHLLPLRSSSSSLERGMHMTSPFTFLEGNTVV 353

RESULT 7
US-09-731-030A-19
; Sequence 19, Application US/09731030A
; Patent No. 6566096
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G
; APPLICANT: GUPTA, Ashwani K.
; APPLICANT: ZASTAWNY, Roman L.
; TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
; FILE REFERENCE: 8074-0015
; CURRENT APPLICATION NUMBER: US/09/731,030A
; CURRENT FILING DATE: 1998-12-29
; PRIOR APPLICATION NUMBER: 60/070,184
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG
US-09-731-030A-19

Query Match          99.8%; Score 1803; DB 2; Length 353;
Best Local Similarity 99.4%; Pred. No. 3.1e-146;
Matches 351; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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RESULT 9

US-08-196-989B-2
; Sequence 2, Application US/08196989B
; Patent No. 5585476
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,989B
; FILING DATE: 15-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MAC-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-196-989B-2

Query Match 90.0%; Score 1625.5; DB 1; Length 352;

Best Local Similarity 89.8%; Pred. No. 4.6e-131; Mismatches 22; Indels 1; Gaps 1;

Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY	1	MGSLYSEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIIVVENLLVLI	60
DB	1	MGGLYSEYLNPEKVOEHYNYTKETLDMQETPSRKVASAFIILCCAIIVVENLLVLI	60
QY	61	NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLS	120
DB	61	NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGVPVTLSTPLQWFAREGSAFITLS	120
QY	121	FSLLAIAERHVAIAKVKLYGSKRCRMLLLIGASWLSISLVGLGILGNCLHLEACS	180
DB	121	NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGVPVTLSTPLQWFAREGSAFITLS	120
QY	121	FSLLAIAERHVAIAKVKLYGSKRCRMLLLIGASWLSISLVGLGILGNCLHLEACS	180
DB	121	FSLLAIAERHVAIAKVKLYGSKRCRMLLLIGASWLSISLVGLGILGNCLHLEACS	180
QY	181	TVLPLAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLLAKTKVTI	240
DB	181	TVLPLAKHYVLCVVTIFSVILLAI VALYVRIYFVVRSSHADVAGQTLLAKTKVTI	240
QY	241	VFTVCWLPAPFISLLLDYACPVHSCPILYKAHYKFAVSTLNSLNPNVIYTWRSRDL	300
DB	241	VFTVCWLPAPFISLLLDYACPVHSCPILYKAHYKFAVSTLNSLNPNVIYTWRSRDL	300
QY	301	RPLQWRPGVGVQRRGGTGGHLLPLRSSSSSLERGMHPTSPTEGNTVV	353
DB	301	RPLQWRPGVGVQRRGGTGGHLLPLRSSSSSLERGMHPTSPTEGNTVV	352

RESULT 10

US-08-760-936-2
; Sequence 2, Application US/08760936
; Patent No. 5856443
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,936
; FILING DATE: December 6, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-760-936-2

Query Match 90.0%; Score 1625.5; DB 1; Length 352;

Best Local Similarity 89.8%; Pred. No. 4.6e-131; Mismatches 22; Indels 1; Gaps 1;

Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY	1	MGSLYSEYLNPNKVOEHYNYTKETLTQETTSRQVASAFIVILCCAIIVVENLLVLI	60
DB	1	MGGLYSEYLNPEKVOEHYNYTKETLDMQETPSRKVASAFIILCCAIIVVENLLVLI	60
QY	61	NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAFITLS	120
DB	61	NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGVPVTLSTPLQWFAREGSAFITLS	120
QY	121	FSLLAIAERHVAIAKVKLYGSKRCRMLLLIGASWLSISLVGLGILGNCLHLEACS	180
DB	121	FSLLAIAERHVAIAKVKLYGSKRCRMLLLIGASWLSISLVGLGILGNCLHLEACS	180
QY	181	TVLPLAKHYVLCVVTIFSIILAI VALYVRIYCVVRSSHADMAAPQTLLAKTKVTI	240
DB	181	TVLPLAKHYVLCVVTIFSVILLAI VALYVRIYFVVRSSHADVAGQTLLAKTKVTI	240
QY	241	VFTVCWLPAPFISLLLDYACPVHSCPILYKAHYKFAVSTLNSLNPNVIYTWRSRDL	300
DB	241	VFTVCWLPAPFISLLLDYACPVHSCPILYKAHYKFAVSTLNSLNPNVIYTWRSRDL	300
QY	301	RPLQWRPGVGVQRRGGTGGHLLPLRSSSSSLERGMHPTSPTEGNTVV	353
DB	301	RPLQWRPGVGVQRRGGTGGHLLPLRSSSSSLERGMHPTSPTEGNTVV	352

RESULT 11

US-09-582-200A-11
; Sequence 11, Application US/09582200A
; Patent No. 6482609

```
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald G.
; APPLICANT: Kamboj, Rajender
; APPLICANT: Peters, Diana
; APPLICANT: Kooshesh, Fatemeh
; APPLICANT: Vyas, Tejal B.
; APPLICANT: Gupta, Ashwani
; TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY RE
; FILE REFERENCE: 108074-00002
; CURRENT APPLICATION NUMBER: US/09/592,200A
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/222,995
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: PCT/CA98/01195
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/109,885
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/080,610
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/070,185
; PRIOR FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 352
; TYPE: PRT
; ORGANISM: rat EDG-4 polypeptide
US-09-582-200A-11

Query Match          90.0%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 4.6e-131;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKVOEHYNYTKETLETQETTSRQVSAFIVILCAIIVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPEKVOEHYNYTKETLDMQETPSRKVASAFIILCCAIIVENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLGPIILGNCLHLEACS 180
Db 121 FSLLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSISLVGLGPIILGNCLHLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSVIILAIVALYVRIYFVVRSSHADVAGPQTALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREV 300
Db 241 VFIIICWLPAPFSLILLDSTCPVRACPVLYKAHYFFAFATLNSLNPVIYTWRSRDLRREV 300

Qy 301 RPLQCRPGVGQVQRRGGTGGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVW 353
Db 301 RPLLCWRQKGATG-RRGNGPGRHLLPLRSSSSSLERGLHMTPTPTFLEGNTVW 352

RESULT 12
US-09-169-205D-24
; Sequence 24, Application US/09169205D
; Patent No. 6485922
; GENERAL INFORMATION:
; APPLICANT: Eriksen, James
; APPLICANT: Goddard, J. Graham
; APPLICANT: Kiefer, Michael
; TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE
; FILE REFERENCE: 252/004
; CURRENT APPLICATION NUMBER: US/09/169,205D
; CURRENT FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 24
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-169-205D-24

Query Match          90.0%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 4.6e-131;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MGSLYSEYLNPNKVOEHYNYTKETLETQETTSRQVSAFIVILCAIIVENLLVLIIVAR 60
Db 1 MGSLYSEYLNPEKVOEHYNYTKETLDMQETPSRKVASAFIILCCAIIVENLLVLIIVAR 60

Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120

Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSISLVGLGPIILGNCLHLEACS 180
Db 121 FSLLAIAIERQVAIAKVKLYGSDKSCRMMLIGASWLSISLVGLGPIILGNCLHLEACS 180

Qy 181 TVLPLYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSSSHADMAAPQTLALLKTTVTIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSVIILAIVALYVRIYFVVRSSHADVAGPQTALLKTTVTIVLG 240

Qy 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLNPVIYTWRSRDLRREV 300
Db 241 VFIIICWLPAPFSLILLDSTCPVRACPVLYKAHYFFAFATLNSLNPVIYTWRSRDLRREV 300

Qy 301 RPLQCRPGVGQVQRRGGTGGHLLPLRSSSSSLERGMHMTPTPTFLEGNTVW 353
Db 301 RPLLCWRQKGATG-RRGNGPGRHLLPLRSSSSSLERGLHMTPTPTFLEGNTVW 352

RESULT 13
US-09-225-024-2
; Sequence 2, Application US/09225024
; Patent No. 6518414
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,024
; FILING DATE: 04-JAN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,936
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/196,989
; FILING DATE: 15-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: MAC-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-225-024-2

Query Match 90.0%; Score 1625.5; DB 2; Length 352;

Best Local Similarity 89.8%; Pred. No. 4.6e-131;

Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

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QY 1 MGSLEYLNPKNKQVEHYNYTKETLETOETTSROVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLEYLNPKNKQVEHYNYTKETLETOETTSROVASAFIVILCCAIIVVENLLVLIAR 60
QY 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY 121 FSLAIAIERQVAIAKVKLYGDKSCRMMLLIGASWLSLVGLGPIGWNCGLHLEACS 180
DB 121 FSLAIAIERQVAIAKVKLYGDKSCRMMLLIGASWLSLVGLGPIGWNCGLHLEACS 180
QY 181 TVLPLAKHYVLCVVTIFSIILAIVALVRYICVVRSSHADMAAPOTLALLKTTVILG 240
DB 181 TVLPLAKHYVLCVVTIFSIILAIVALVRYICVVRSSHADMAAPOTLALLKTTVILG 240
QY 241 VFVLCWLPAPFSLILLDYACPVHSCPTLYKAHYKFAVSTLNSLLNPVITWRSRDLRREVL 300
DB 241 VFVLCWLPAPFSLILLDYACPVHSCPTLYKAHYKFAVSTLNSLLNPVITWRSRDLRREVL 300
QY 301 RPLQCRPQGVQGRRGTPGHLLPLRSSSLRSGMMPSPFTFLEGTNV 353
DB 301 RPLQCRPQGVQGRRGTPGHLLPLRSSSLRSGMMPSPFTFLEGTNV 353
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RESULT 14

US-09-262-477-2

Sequence 2, Application US/09262477A

Patent No. 6423508

GENERAL INFORMATION:

APPLICANT: George Livi

APPLICANT: Derek Bergsma

APPLICANT: Jeffrey Stadel

APPLICANT: Winnie Chan

APPLICANT: Randall Johnson

APPLICANT: Shelagh Wilson

APPLICANT: Jon Chambers

APPLICANT: Philippe Robert

APPLICANT: Nassirah Khandoudi

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDE SEQUENCES OF HUMAN EDG-1C AND

TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND ANTAGONISTS FOR HUMAN

TITLE OF INVENTION: EDG-1C RECEPTOR AND SPHINGOSINE 1-PHOSPHATE LIGAND AND

TITLE OF INVENTION: INTERACTION THEREOF

FILE REFERENCE: GP50006

CURRENT APPLICATION NUMBER: US/09/262,477A

CURRENT FILING DATE: 1999-03-04

EARLIER APPLICATION NUMBER: 60/077,369

EARLIER FILING DATE: 1998-03-09

EARLIER APPLICATION NUMBER: 60/087,102

EARLIER FILING DATE: 1998-05-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 382

TYPE: PRT

ORGANISM: Human

US-09-262-477-2

Query Match

Best Local Similarity 47.0%; Score 849; DB 2; Length 382;

Matches 168; Conservative 60; Mismatches 103; Indels 14; Gaps 4;

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Matches 160; Conservative 59; Mismatches 84; Indels 12; Gaps 2;
QY 3 SLYSEYLNPNKQVEHYNYTKETLETOETTSROVASAFIVILCCAIIVVENLLVLIAR 61
DB 14 SSVSDYVNDYDIIVRHNYTGKLNISADRENSIKLTSVVFILCCFIENIFVLTIWKT 73
QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 121
DB 74 KKFHRPMYVFIENLALS DLLAGVAYTANLLSGATYKLTTPAQWFLREGSMFVALSASF 133
QY 122 SLLAIAIERHVAIAKVKLYGDKSCRMMLLIGASWLSLVGLGPIGWNCGLHLEACS 181
DB 134 SLLAIAIERYITMLKMKLNGSNRFLFLISACWVISLILGGLPIMGWNCISALSSCST 193
QY 182 VLPLAKHYVLCVVTIFSIILAIVALVRYICVVRSSHADMAAPOTLALLKTTVILG 230
DB 194 VLPLAKHYVLCVVTIFSIILAIVALVRYICVVRSSHADMAAPOTLALLKTTVILG 230
QY 231 LLKTVIIVLGVFIVCWLPAFSLILLDYACPVHSCPTLYKAHYKFAVSTLNSLLNPVITW 290
DB 254 LLKTVIIVLGVFIVCWLPAFSLILLDYACPVHSCPTLYKAHYKFAVSTLNSLLNPVITW 290
QY 291 RSRDLRREVLRLPLOC 305
DB 314 TNKEMRRAFIRIMSC 328
```

RESULT 15

US-08-196-989B-4

Sequence 4, Application US/08196989B

Patent No. 5585476

GENERAL INFORMATION:

APPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of

TITLE OF INVENTION: G-Protein Coupled Receptors

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/196,989B

FILING DATE: 15-FEB-1994

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lloyd, Jeff

REGISTRATION NUMBER: 35,589

REFERENCE/DOCKET NUMBER: MAC-100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 383 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-196-989B-4

Query Match

Best Local Similarity 46.9%; Score 847; DB 1; Length 383;

Matches 168; Conservative 60; Mismatches 103; Indels 14; Gaps 4;

QY 3 SLYSEYLNPNKQVEHYNYTKETLETOETTSROVASAFIVILCCAIIVVENLLVLIAR 61

Db 15 SQVSDYGNVDIIVRHNYVTGKLNIGVEKDHGKLTSSVVFILICLIILENIFVLLTIWKT 74
Qy 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
Db 75 KKFHRPMYFFIGNLALSDDLAVAYTANLLLSGATTYKLTPAQWFLREGSMFVALSASVF 134
Qy 122 SLLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLLISLVGGLPILGWNCIGHLEACST 181
Db 135 SLLAIAIERIYTMLKKUHGNSRSRSELLISACWVLSLIILGGUPIMGWNCISSLSCST 194
Qy 182 VLPLYAKHYVLCVVTIFSIILLAIIVALYVRIYCVVRS-----SHADMAAPOTLA 230
Db 195 VLPLYKHYYILFCTTVFTLLLSIVILYCRYSLVRTSRRLTFRKNISKASRSSEKSLA 254
Qy 231 LLKTVTIVLGVFTVVCWLPAFSILLDDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTW 290
Db 255 LLKTVIIVLSVFIACWAPLFIILLIDVGCKARTCDILYKAHYFLVLAIVNSGTNPVIYTL 314
Qy 291 RSRDLRREVLRPLQWR-PGVGVQGR-RRGGTPGHLLPLRSSSS 333
Db 315 TNKEMRRAFIRIISCCKCPNGDSAGKFKRPIIPGMFERSRSDNS 359

Search completed: December 4, 2005, 06:24:23
Job time : 35.5 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:38:02 ; Search time 152 Seconds
(without alignments)
1638.497 Million cell updates/sec

Title: US-10-084-507B-17

Perfect score: 1806

Sequence: 1 MGSLYSEVLPNPKVQEHYNY.....LERGMHMTPTFLRGNTVV 353

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1804	99.9	353	1	EDG5 HUMAN	O95136 homo sapien
2	1631.5	90.3	352	2	O8C3Q7_MOUSE	O8C3Q7 m mus muscu
3	1625.5	90.0	352	1	EDG5 RAT	P47752 rattus norv
4	1625.5	90.0	352	2	O54A16_RAT	O54A16 rattus norv
5	1622.5	89.8	352	1	EDG5 MOUSE	P52592 mus musculus
6	998	55.3	370	1	EDG5 BRARE	O918k8 brachydanio
7	933	51.7	202	2	O91XR0_CAVPO	O91XR0 cavia porce
8	859	48.1	190	2	O9ESK0_RAT	O9ESK0 rattus norv
9	856	47.4	382	2	Q5R7A1_PONPY	Q5R7A1 pongo pygma
10	849	47.0	382	2	O9NYN8_HUMAN	O9NYN8 homo sapien
11	847	46.9	383	1	EDG1 RAT	P48303 rattus norv
12	847	46.9	383	2	Q4V7F6_RAT	Q4V7F6 rattus norv
13	845	46.8	382	2	O9DC35_MOUSE	O9DC35 m mus muscu
14	844	46.7	382	2	O5B1P0_BOVIN	O5B1P0 bos taurus
15	841	46.6	373	2	Q4T9E2_TETNG	Q4T9E2 tetraodon n
16	839	46.5	382	1	EDG1 MOUSE	O08530 mus musculus
17	837	46.3	375	2	O5U389_BRARE	O5U389 brachydanio
18	837	46.3	382	2	O5E9P3_BOVIN	O5E9P3 bos taurus
19	836.5	46.3	381	1	EDG1 HUMAN	P21453 homo sapien
20	835	46.2	374	2	O6GLU6_XENLA	O6GLU6 xenopus lae
21	822.5	45.5	326	2	O99NR8_CASCN	O99NR8 castor cana
22	820.5	45.4	325	2	Q71BN5_OTOGA	Q71BN5 otollemur ga
23	819	45.3	325	2	O9BF55_ARTJA	O9BF55 artibeus ja
24	817	45.2	362	1	EDG1 BRARE	O9DDK4 brachydanio
25	816.5	45.2	326	2	O6JC76_9EUTH	O6JC76 solenodon p
26	816.5	45.2	326	2	O9BF73_CONCR	O9BF73 condylura c
27	816.5	45.2	326	2	O99NR0_HYST	O99NR0 cavia teschu
28	816.5	45.2	326	2	O99NR4_HYSBR	O99NR4 hystrix bra
29	816	45.2	326	2	O8MK87_TADBR	O8MK87 tadaria br
30	815.5	45.2	326	2	O99NQ7_AGOTA	O99NQ7 agouti tacz
31	814	45.1	326	2	O99NR1_HETGA	O99NR1 heteroceph

32 813.5 45.0 326 2 Q9BF72_SORAR Q9BF72 sores arane
33 813.5 45.0 326 2 O99NQ9_HYDHY Q99NQ9 hydrochoeru
34 813.5 45.0 326 2 O99NR3_EREDO Q99NR3 erethizon d
35 812.5 45.0 326 2 O9BF75_MYRTR Q9BF75 myrmecophag
36 812.5 45.0 326 2 Q9BF76_TAMTE Q9BF76 tamandua te
37 811.5 44.9 326 2 Q9BF74_ERICO Q9BF74 erinaceus c
38 811.5 44.9 326 2 O9BF79_CHOHO Q9BF79 choloepus h
39 811.5 44.9 326 2 O99NR5_MOUSE Q99NR5 mus musculus
40 811 44.9 292 2 O91XR2_CAVPO Q91XR2 cavia porce
41 809.5 44.8 325 2 O99NR9_TAMST Q99NR9 tamias stri
42 807.5 44.7 326 2 O8MK86_MEGLY Q8MK86 megaderma l
43 807.5 44.7 326 2 Q9BF66_ELERU Q9BF66 elephantulu
44 806.5 44.7 326 2 Q9BF65_ORYAF Q9BF65 orycteropus
45 805.5 44.6 325 2 Q9BF41_PANON Q9BF41 panthera on

ALIGNMENTS

RESULT 1
EDG5_HUMAN
ID EDG5_HUMAN STANDARD; PRT; 353 AA.
AC O95136; O8CUN8;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
DE (Endothelial differentiation G-protein coupled receptor 5)
DE (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Name=EDG5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX PubMed=10617617; DOI=10.1074/jbc.275.1.288;
RA An S., Zheng Y., Bleu T.;
RT "Sphingosine 1-phosphate-induced cell proliferation, survival, and
RT related signaling events mediated by G protein-coupled receptors Edg3
RT and Edg5.";
RL J. Biol. Chem. 275:288-296(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Receptor for the lysophospholipid sphingosine 1-
 CC phosphate (S1P). S1P is a bioactive lysophospholipid that elicits
 CC diverse physiological effect on most types of cells and tissues.
 CC When expressed in rat HTC4 hepatoma cells, is capable of mediating
 CC S1P-induced cell proliferation and suppression of apoptosis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AF034780; AAC98919.1; -; mRNA.
 DR EMBL; AY262688; AAP20652.1; -; Genomic_DNA.
 DR EMBL; BC069598; AAH69598.1; -; mRNA.
 DR Ensembl; ENSG00000175898; Homo sapiens.
 DR HGNC; HGNC:3169; EDG5.
 DR MIM; 605111; .
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0008289; F:lipid binding; TAS.
 DR GO; GO:0008289; P:activation of MAPK; TAS.
 DR GO; GO:000187; P:G-protein coupled receptor protein signalin. .; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR InterPro; IPR004063; EDG5 receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR0004061; S1P_receptor.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR01525; EDG5RECEPTOR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PRINTS; PR01523; S1PRECEPTOR.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein;
 KW Multigene family; Palmitate; Receptor; Transducer; Transmembrane.
 FT TOPO_DOM 1 34
 FT Extracellular (Potential).
 FT TRANSMEM 35 59
 FT TOPO_DOM 60 66
 FT TRANSMEM 67 95
 FT TOPO_DOM 96 109
 FT Extracellular (Potential).
 FT TRANSMEM 110 128
 FT TOPO_DOM 129 147
 FT Cytoplasmic (Potential).
 FT TRANSMEM 148 173
 FT TOPO_DOM 174 189
 FT Extracellular (Potential).
 FT TRANSMEM 190 210
 FT TOPO_DOM 211 233
 FT Cytoplasmic (Potential).
 FT TRANSMEM 234 255
 FT TOPO_DOM 256 271
 FT Extracellular (Potential).
 FT TRANSMEM 272 292
 FT TOPO_DOM 293 305
 FT Cytoplasmic (Potential).
 FT LIPID 305 305
 FT CARBOHYD 19 19
 FT N-linked (GlcNAc. .) (Potential).
 FT CONFLICT 113 113
 FT F -> S (in Ref. 1).
 FT CONFLICT 318 318
 FT G -> V (in Ref. 1).
 SQ SEQUENCE 353 AA; 38867 MW; 8E37084284B7E8 CRC64;
 Query Match 99.9%; Score 1804; DB 1; Length 353;
 Best Local Similarity 99.7%; Pred. No. 1.8e-115;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGSLYSEYLNPNKQVHNYTETLETQTTTSQVASFIVILCAIVVNNLLVLIAR 60
 DB 1 MGSLYSEYLNPNKQVHNYTETLETQTTTSQVASFIVILCAIVVNNLLVLIAR 60
 QY 61 NSKFHSAMVLFGLNLAASDLLAGVAVNTLLSGSVTLRLTPVQVFAREGSAFILTASV 120
 DB 61 NSKFHSAMVLFGLNLAASDLLAGVAVNTLLSGSVTLRLTPVQVFAREGSAFILTASV 120
 QY 121 FSLLAIAIERHVAIAKVLKYGSKRCMLLLIGASWLSLVLGGLPILGNWNCGLHLEACS 180
 DB 121 FSLLAIAIERHVAIAKVLKYGSKRCMLLLIGASWLSLVLGGLPILGNWNCGLHLEACS 180

QY 181 TVLPYAKHYVLCVVTIFSIILLAIYALYRIYCVWRSSHADMAAPOTLALKTTVI 240
 DB 181 TVLPYAKHYVLCVVTIFSIILLAIYALYRIYCVWRSSHADMAAPOTLALKTTVI 240
 QY 241 VFIVCWLPAFASILLDDYACPVHSCPILYKAHYXFAVSTLSLNPVIYTWRSRLR 300
 DB 241 VFIVCWLPAFASILLDDYACPVHSCPILYKAHYXFAVSTLSLNPVIYTWRSRLR 300
 QY 301 RPLQWRPGVGVQRRGGTGFHLLPLRSSSLRGMHMTSPFTLEGNTVV 353
 DB 301 RPLQWRPGVGVQRRGGTGFHLLPLRSSSLRGMHMTSPFTLEGNTVV 353
 RESULT 2
 Q8C307_MOUSE
 ID Q8C307_MOUSE PRELIMINARY; PRT; 352 AA.
 AC Q8C307;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
 DE library, clone:D430039A03 product:endothelial differentiation,
 DE sphingolipid G-protein-coupled receptor, 5, full insert sequence
 DE (Endothelial differentiation, sphingolipid G-protein-coupled receptor,
 DE 5).
 GN Name=Edg5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Washima J., Mazzarelli J., Wombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 403:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RA The FANTOM Consortium,
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes."
RN Genome Res. 10:1617-1630(2000).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu M., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -l- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AK085114; BAC39268.1; -; mRNA.
DR EMBL; BC096760; AAH96760.1; -; mRNA.
DR Ensembl; ENSMUSG00000043895; Mus musculus.
DR MGI; MGI:99569; Edg5.
DR GO; GO:0007610; P:behavior; IMP.
DR InterPro; IPR004063; EDG5 receptor.
DR InterPro; IPR000276; GPCR_Rhodpn.
DR InterPro; IPR004061; S1P_receptor.

DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS0262; G-PROTEIN_RECEPTOR; Transducer; Transmembrane.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 38829 MW; 6A3E426B0FE54406 CRC64;
Query Match 90.3%; Score 1631.5; DB 2; Length 352;
Best Local Similarity 90.4%; Pred. No. 1.1e-103;
Matches 319; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
QY 1 MGSLSYSEYNPNKQVHYNYTKETLETTSTSRQVASFVILCCAIIVENLLVLIIVAR 60
Db 1 MGGLSEYNLPKLVLEHYNYTKETLDMQETTSRKVASAFIILCCAIIVENLLVLIIVAR 60
QY 61 NSKFHSAWYFLGNLAASDLGAVAFVANTLLSGVTLRLTPVQVFAREGSAFILTASV 120
Db 61 NSKFHSAWYFLGNLAASDLGAVAFVANTLLSGVTLRLTPVQVFAREGSAFILTASV 120
QY 121 FSLAIAIAERHVAIAKVLGYGSKSCRMILLIGASWLSLVLLGGLPILGWNCLGLEACS 180
Db 121 FSLAIAIAERQVALAKVLGYGSKSCRMILLIGASWLSLVLLGGLPILGWNCLGLEACS 180
QY 181 TVLPLYAKHYVLCVVTFISIIILAIYALYVRIYCVVRSHADMAAPOTLALKTTVILG 240
Db 181 TVLPLYAKHYVLCVVTFISVILLAIYALYVRIYFVRSHADVAGPQTALLKTTVILG 240
QY 241 VFIICWLPAPFSLILLDSTCPVACPVLYKHYFAFATLNSLLNPIVYTWRSRDLRREVL 300
Db 241 VFIICWLPAPFSLILLDSTCPVACPVLYKHYFAFATLNSLLNPIVYTWRSRDLRREVL 300
QY 301 RPLQWRGVGVQGRGRTGPHLLPLRSSSLRGMHMTSPFTLEGNVTV 353
Db 301 RPLQWRGVGVQGRGRTGPHLLPLRSSSLRGMHMTSPFTLEGNVTV 352
RESULT 3
EDGS_RAT STANDARD; PRT; 352 AA.
AC P47752;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5) (G-protein
DE coupled receptor H218) (AGRI6) (Endothelial differentiation G-protein
DE coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2).
GN Name=Edg5;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain, and Lung;
RX MEDLINE=94373324; PubMed=8087418; DOI=10.1006/mcne.1994.1024;
RA MacLennan A.J., Browe C.S., Gaskin A.A., Lado D.C., Shaw G.;
RT "Cloning and characterization of a putative G-protein coupled receptor
RT potentially involved in development."
RL Mol. Cell. Neurosci. 5:201-209(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aortic smooth muscle;
RX MEDLINE=93176155; PubMed=8382486;
RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
RA Takawa Y.;
RT "Molecular cloning of a novel putative G protein-coupled receptor
RT expressed in the cardiovascular system."
RL Biochem. Biophys. Res. Commun. 190:1104-1109(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;

RX MEDLINE=98072391; PubMed=9409733; DOI=10.1016/S0014-5793(97)01301-X;
RA An S., Bleu T., Huang W., Hallmark O.G., Coughlin S.R., Goetzl E.J.;
RT "Identification of cDNAs encoding two G protein-coupled receptors for
RL lysophospholipids."; *FEBS Lett.* 417:279-282 (1997).
RN [4]
RP PHARMACOLOGICAL CHARACTERIZATION.
RX PubMed=10383399; DOI=10.1074/jbc.274.27.18997;
RA Ancellin N., Hla T.;
RT "Differential pharmacological properties and signal transduction of
RT the sphingosine 1-phosphate receptors EDG-1, EDG-3, and EDG-5."; *J.
RL J. Biol. Chem.* 274:18997-19002 (1999).
CC -!- FUNCTION: Receptor for the lysophospholipid that elicits
CC phosphate (SIP). SIP is a bioactive lysophospholipid that elicits
CC diverse physiological effect on most types of cells and tissues.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in all developing tissues with
CC highest levels detected in primitive, transformed cells. Relative
CC abundance: lung > kidney = skin > gut > spleen > brain > liver.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U10699; AA19241.1; -; mRNA.
DR EMBL; AF022138; AAC53494.1; -; mRNA.
DR PIR; JC1465; JC1465.
DR Ensembl; ENSRNOG0000020653; Rattus norvegicus.
DR RGD; 68334; Edg5
DR GO; GO:0004930; F:G-protein coupled receptor activity; IDA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; SIP_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01523; SIPRECEPTOR.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PRINTS; PR01523; SIPRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
KW Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 34 Extracellular (Potential).
FT TRANSMEM 35 59 1 (Potential).
FT TOPO_DOM 60 66 Cytoplasmic (Potential).
FT TRANSMEM 67 95 2 (Potential).
FT TOPO_DOM 96 109 Extracellular (Potential).
FT TRANSMEM 110 128 3 (Potential).
FT TOPO_DOM 129 147 Cytoplasmic (Potential).
FT TRANSMEM 148 173 4 (Potential).
FT TOPO_DOM 174 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 233 Cytoplasmic (Potential).
FT TRANSMEM 234 255 6 (Potential).
FT TOPO_DOM 256 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT TOPO_DOM 293 352 Cytoplasmic (Potential).
FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
FT CARBOHYD 19 19 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 90.0%; Score 1625.5; DB 1; Length 352;
Best Local Similarity 89.8%; Pred. No. 2.9e-103;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLYSEVLNPNKQVQEHYNTKETLEQTTSRQVASFIVILCAIIVENLLVLIIVAR 60
DB 1 MGGLYSEVLNPNKQVQEHYNTKETLEQTTSRQVASFIVILCAIIVENLLVLIIVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
|||||

Db 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
QY 121 FSLAIAIERHVAIAKVKLYGSKDSKMLLIGASWLSISLVGLPILGNCLGHLEACS 180
DB 121 FSLAIAIERHVAIAKVKLYGSKDSKMLLIGASWLSISLVGLPILGNCLGHLEACS 180
QY 181 TVLPYAKHYVLCVVTTFISIIILAIIVLYVRIYCVWRSSHADMAAPOTLALKKTVTIVLG 240
DB 181 TVLPYAKHYVLCVVTTFISIIILAIIVLYVRIYCVWRSSHADVAGPQTALLKKTVTIVLG 240
QY 241 VFIICWLPAPFISILLDYACPVHSCPIIYKHAHYXFAVSTLSLLNPVIYTWRSRDLRREV 300
DB 241 VFIICWLPAPFISILLDYACPVHSCPIIYKHAHYXFAVSTLSLLNPVIYTWRSRDLRREV 300
QY 301 RPLQWRPGVQVQRRGGTFCGHLLPLRSSSLERGHMPTSTFLEGNTVV 353
DB 301 RPLLCWRQKGATG-RRGGNPGHRLPLRSSSLERGLHMPSTPTFLEGNTVV 352

RESULT 4
Q54A16 RAT PRELIMINARY; PRT; 352 AA.
ID Q54A16 RAT PRELIMINARY; PRT; 352 AA.
AC Q54A16;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE AGR16.
GN Name=AGR16;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RX MEDLINE=93176155; PubMed=8382486;
RA Okazaki H., Ishizaka N., Sakurai T., Kurokawa K., Goto K., Kumada M.,
RA Takuwa Y.;
RT "Molecular cloning of a novel putative G protein-coupled receptor
RT expressed in the cardiovascular system."; *FEBS Lett.* 352:1104-1109 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
RA Gonda K., Takuwa Y.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
EMBL; AB016931; BAA32454.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; SIP_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PRINTS; PR01523; SIPRECEPTOR.
KW PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 352 AA; 38735 MW; 9C933A18E756CE1E CRC64;

Query Match 90.0%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 2.9e-103;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGSLYSEVLNPNKQVQEHYNTKETLEQTTSRQVASFIVILCAIIVENLLVLIIVAR 60
DB 1 MGGLYSEVLNPNKQVQEHYNTKETLEQTTSRQVASFIVILCAIIVENLLVLIIVAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQVFAREGSAFTLSASV 120
|||||

Db 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLOWFAREGSFATLSASV 120
 Qy 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGNCLHLEACS 180
 Db 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGNCLHLEACS 180
 Qy 181 TVPLYAKHYLVLCVVTIFSIILLAIIVLVYVYVVRSSHADVAAPQTLALKKTIVTVLG 240
 Db 181 TVPLYAKHYLVLCVVTIFSVILLAIIVLVYVYVVRSSHADVAGPQTLALKKTIVTVLG 240
 Qy 241 VFIVCWLPFAFSLILLDYACPVHSCPTLYKHAHYKFAVSTLNSLLNPVYVYVVRSSHADVAAPQTLALKKTIVTVLG 300
 Db 241 VFIIICWLPFAFSLILLDSTCPVACPVLYKHAHYFFAFATLNSLLNPVYVYVVRSSHADVAAPQTLALKKTIVTVLG 300
 Qy 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLERGMHMTSPTEFLENTVV 353
 Db 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLERGMHMTSPTEFLENTVV 352

RESULT 5
 EDG5_MOUSE STANDARD; PRT; 352 AA.
 AC P5252; Q9R236;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
 DE (lysophospholipid receptor B2) (Endothelial differentiation G-protein coupled receptor 5) (Sphingosine 1-phosphate receptor 2) (S1P2).
 GN Names=Edg5; Synonyms=Gpcr13, Lpb2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND TISSUE SPECIFICITY.
 RC STRAIN=129/SvJ;
 RC MEDLINE=9913230; PubMed=9931453; DOI=10.1016/S0378-1119(98)00589-7;
 RA Zhang G., Contos J.J.A., Weiner J.A., Fukushima N., Chun J.;
 RT "Comparative analysis of three murine G-protein coupled receptors activated by sphingosine-1-phosphate.";
 RL Gene 227:89-99(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 62-241.
 RC TISSUE=Testis;
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RA Copeland N.G., Jenkins N.A.;
 RT "Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptors.";
 RL Genomics 18:175-184(1993).
 CC -1- FUNCTION: Receptor for the lysophospholipid sphingosine 1-phosphate (S1P). S1P is a bioactive lysophospholipid that elicits diverse physiological effect on most types of cells and tissues.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Most abundant in heart and lung; low, but clearly observed in kidney, liver and thymus; much lower but detectable in brain, testis, stomach and intestine. Not significantly detected in any of the sections of embryonic day (E) 14-18, except in embryonic brain.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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 CC -----
 CC ENBL; AF108020; AAD16976.1; -; Genomic_DNA.
 CC ENBL; L20334; AAA16846.1; -; mRNA.
 CC PIR; E48909; E48909.
 CC Ensembl; ENSMUSG00000043895; Mus musculus.

DR MGI; 99569; Edg5.
 GO; GO:0007610; P:behavior; IMP.
 DR InterPro; IPR004063; EDG5 receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR004061; S1P_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01525; EDG5RECEPTOR.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PRINTS; PR01523; S1PRECEPTOR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PARTIAL.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
 FT TOPO_DOM 1 34 Extracellular (Potential).
 FT TRANSMEM 35 59 1 (Potential).
 FT TOPO_DOM 60 66 Cytoplasmic (Potential).
 FT TRANSMEM 67 95 2 (Potential).
 FT TOPO_DOM 96 109 Extracellular (Potential).
 FT TRANSMEM 110 128 3 (Potential).
 FT TOPO_DOM 129 147 Cytoplasmic (Potential).
 FT TRANSMEM 148 173 4 (Potential).
 FT TOPO_DOM 174 199 Extracellular (Potential).
 FT TRANSMEM 190 210 5 (Potential).
 FT TOPO_DOM 211 233 Cytoplasmic (Potential).
 FT TRANSMEM 234 255 6 (Potential).
 FT TOPO_DOM 256 271 Extracellular (Potential).
 FT TRANSMEM 272 292 7 (Potential).
 FT TOPO_DOM 293 305 Cytoplasmic (Potential).
 FT LIPID 305 305 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 19 19 N-linked (GlcNAc..) (Potential).
 FT CONFLICT 166 166 P -> S (in Ref. 2).
 FT CONFLICT 175 175 Q -> K (in Ref. 2).
 FT CONFLICT 189 189 H -> R (in Ref. 2).
 SQ SEQUENCE 352 AA; 38871 MW; 9A3E456DD488FE6B CRC64;
 Query Match 89.8%; Score 1622.5; DB 1; Length 352;
 Best Local Similarity 90.1%; Pred. No. 4.6e-103;
 Matches 318; Conservative 12; Mismatches 22; Indels 1; Gaps 1;
 QY 1 MGSLYSEYLNPNKQVHEHYNYTKETLTQETTSQVASFIVILCCAIIVVENLLVLIAR 60
 DB 1 MGGLYSEYLNPEKVLHEHYNYTKETLDMQETTSRKVASAFIILCCAIIVVENLLVLIAR 60
 QY 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFATLSASV 120
 DB 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGHVTLSLTPVQWFAREVSFAFIIISASV 120
 QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGNCLHLEACS 180
 DB 121 FSLLAIAIERQVALAKVKLYGSDKSCRMILLIGASWLSLVGLGPIILGNCLHLEACS 180
 QY 181 TVPLYAKHYLVLCVVTIFSIILLAIIVLVYVYVVRSSHADVAAPQTLALKKTIVTVLG 240
 DB 181 TVPLYAKHYLVLCVVTIFSVILLAIIVLVYVYVVRSSHADVAGPQTLALKKTIVTVLG 240
 QY 241 VFIVCWLPFAFSLILLDYACPVHSCPTLYKHAHYKFAVSTLNSLLNPVYVYVVRSSHADVAAPQTLALKKTIVTVLG 300
 DB 241 VFIIICWLPFAFSLILLDSTCPVACPVLYKHAHYFFAFATLNSLLNPVYVYVVRSSHADVAAPQTLALKKTIVTVLG 300
 QY 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLERGMHMTSPTEFLENTVV 353
 DB 301 RPLQWRPGVGVQRRRGCTPGHLLPLRSSSLERGMHMTSPTEFLENTVV 352
 RESULT 6
 EDG5_BRARE STANDARD; PRT; 370 AA.
 ID EDG5_BRARE
 AC Q918K8;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Sphingosine 1-phosphate receptor Edg-5 (S1P receptor Edg-5)
 DE (Sphingosine 1-phosphate receptor 2) (S1P2).

GN Name=edg5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS MIL HIS-150 AND CYS-167.
RX MEDLINE=20365730; PubMed=10910360; DOI=10.1038/35018092;
RA Kupperman E., An S., Osborne N., Waldron S., Stainier D.Y.R.;
RT "A sphingosine-1-phosphate receptor regulates cell migration during
RL Nature 406:192-195 (2000).
CC -!- FUNCTION: Receptor for the lysophingolipid sphingosine 1-
CC phosphate (SIP). SIP receptor is critical for cell migration and
CC epithelial integrity during vertebrate embryogenesis.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: The expression pattern is complex and
CC dynamic. Maternal expression is found in a diffuse pattern
CC throughout the blastoderm, and this pattern persists through the
CC onset of gastrulation. More pronounced expression can be seen at
CC tailbud stage in the anterior portion of the embryo and along the
CC midbrain/hindbrain boundary and the tip of the tail where blisters
CC later develop in receptor mutants. At the 18-somite stage,
CC expression appears just lateral to the midline, and as the
CC myocardial precursors migrate to the midline, their location
CC overlaps with this domain of receptor expression.
CC -!- DISEASE: Defects in edg5 are a cause of heart development
CC abnormality named miles apart (mil). In all vertebrates, the
CC myocardial progenitors involute early during gastrulation and come
CC to occupy bilateral positions in the anterior lateral plate and
CC mesoderm (fpm). During somitogenesis, these cells undergo a second
CC phase of migration toward the midline and fuse to form the
CC definitive heart tube. Defects in EDG5 disrupt this process,
CC leading to the formation of two laterally positioned hearts
CC (cardia bifida). The mil phenotype for which two recessive alleles
CC exist, mil(m93) and mil(te273) are fully penetrant.
CC Mil(m93)/mil(te273) transheterozygous embryos display the same
CC phenotype as homozygotes for either single mutant allele. In
CC addition to cardia bifida, mil mutants display epithelial tail
CC blisters, indicative of a defect in epithelial integrity.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AF260256; AAF88001.1; -, mRNA.
CC Ensembl; ENSDARG00000009719; Danio rerio.
CC ZFIN; ZDB-GENE-020123-2; edg5.
CC InterPro; IPR000987; EDG1receptor.
CC InterPro; IPR000276; GPCR Rhodopsin.
CC InterPro; IPR004061; SIP_receptor.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00642; EDG1RECEPTOR.
CC PRINTS; PR00237; GPCRRHODOPSN.
CC PRINTS; PR01523; SIPRECEPTOR.
CC PROSITE; PS00237; G PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS00262; G PROTEIN RECEPTOR F1_2; 1.
CC Disease mutation; G-protein coupled receptor; Glycoprotein;
CC Lipoprotein; Palmitate; Receptor; Transducer; Transmembrane.
CC TOPO_DOM 1 57 Extracellular (Potential).
CC TRANSMEM 58 78 1 (Potential).
CC FT TOPO_DOM 79 87 Cytoplasmic (Potential).
CC FT TRANSMEM 88 108 2 (Potential).
CC FT TOPO_DOM 109 128 Extracellular (Potential).
CC TRANSMEM 129 149 3 (Potential).
CC FT TOPO_DOM 150 167 Cytoplasmic (Potential).
CC TRANSMEM 168 188 4 (Potential).
CC FT TOPO_DOM 189 214 Extracellular (Potential).

FT	TRANSMEM	215	235	5 (Potential).
FT	TOPO_DOM	236	254	Cytoplasmic (Potential).
FT	TRANSMEM	255	275	6 (Potential).
FT	TOPO_DOM	276	289	Extracellular (Potential).
FT	TRANSMEM	290	310	7 (Potential).
FT	TOPO_DOM	311	370	Cytoplasmic (Potential).
FT	LIPID	325	325	S-palmitoyl cysteine (By similarity).
FT	CARBOHYD	24	24	N-linked (GlcNAc...) (Potential).
FT	VARIANT	150	150	R -> H (in mil; allele m93; lack of SIP-mediated signaling).
FT	VARIANT	167	167	R -> C (in mil; allele te273; lack of SIP-mediated signaling).
FT	SEQUENCE	370 AA;	41777 MW;	8C6B3A06DEEA6757 CRC64;

Query Match 55.3%; Score 998; DB 1; Length 370;
Best Local Similarity 58.5%; Pred. No. 2.4e-60;
Matches 200; Conservative 51; Mismatches 73; Indels 18; Gaps 4;

QY	3	SLYSEYLNPNKVQEHVNYTKE-----TLETQETTSRQVASAFIVILCCAIIVVENLLV	54
DB	17	SKYQYFNKTLIQVHYLTAKETAEELRDRIKSLSS--LNILFVVICIIILENLLV	74
QY	55	LIIVARNKFSHSMYFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSFI	114
DB	75	LIIVFRNKKFHSAMFFIGNLAFSDLLAGSAYIANIFLSGRTFHLTPVQFIREGTAFI	134
QY	115	TLSASVFSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLISLVGLGPIIGWNCIG	174
DB	135	ALSASVFSLLAIAIERVIAITKVKYGSNKTCTRMFLITGACWMSILGLPIIGWNCIN	194
QY	175	HLEACSTVLPYAKHYVLCVVTIFSIITLLAVALVYRIVCVVSSHADMAAPQTALAKT	234
DB	195	NLDSCSAVLPLNTRYIRFVVTFISIIISLVILYRIVLYRIVTSHQATNSPAVALKT	254
QY	235	VTIVGLVFIVCWLPAFSILLDYACPVHSCPILYKAHYXFAVSTLNSLNLNPIVYVTRSD	294
DB	255	VTIVGLVFIIICWLPAFTILLDTCKMKQCPILNAGIFFFSFATLNSALNPLIYLRSD	314
QY	295	LRREVLRLPQWRGVGVQRRRGTPGHH-LLPIRSSSSLE	335
DB	315	MRKEFLRLCCW-----GLLNCGRPPHRCWPLKSSSSME	349

RESULT 7
Q91XR0_CAVPO
ID Q91XR0_CAVPO PRELIMINARY; PRT; 202 AA.
AC Q91XR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endothelial differentiation sphingolipid G-protein-coupled receptor 5
DE (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L., Cowles R.A., Turner D.J., Logsdon C.D.,
RA Mulholland M.W.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289992; AAK83087.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004063; EDG5_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; SIP_receptor.
DR Pfam; PF00001; 7tm1; 1.

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DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 21836 MW; D9814EC85B42320A CRC64;

Query Match 51.7%; Score 933; DB 2; Length 202;
Best Local Similarity 91.6%; Pred. No. 3.8e-56;
Matches 185; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 20 YKTEILETQETTSRQVASAFIVLCCAIIVENLLVLIIVARNKESAMYLFLGNLAASD 79
DB 1 YKTELDVRETTSRQVASAFIVLCCAIIVENLLVLIIVARNKESAMYLFLGNLAASD 60

QY 80 LLGAVAFVANTLLSGSVTLRLTPVOWFAREGSFATLSASVFSLLAIAIERHVAIAKVKL 139
DB 61 LLGAVAFIANTLLSGSVTLRLTPVOWFAREGSFATLSASVFSLLAIAIERHVAIAKVKL 120

QY 140 YGSDKSCRMLLIGASWLSLVGLPILGWNCLGHLACSTVPLPYAKHYVLCVVTIPS 199
DB 121 YGSDKSCRMLLIGASWLSLVGLPILGWNCLGHLACSTVPLPYAKHYVLCVVTIPS 180

QY 200 ILLAIVAIYVRIYCVRRSSHA 221
DB 181 VILLAIWLVRIYCVRRSSHA 202

RESULT 8
Q9ESKO RAT PRELIMINARY; PRT; 190 AA.
AC Q9ESKO;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative G-protein coupled receptor (fragment).
GN Name=GPCR18;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley/Hsd;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090995; AAG24259.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004063; EDG5 receptor.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01525; EDG5RECEPTOR.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PROSITE; PR01523; S1PRECEPTOR.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 190
SQ SEQUENCE 190 AA; 20718 MW; 3CA0A5C188F168B1 CRC64;

Query Match 48.1%; Score 869; DB 2; Length 190;
Best Local Similarity 88.9%; Pred. No. 8.6e-52;
Matches 169; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 94 GSVTLRLTPVOWFAREGSFATLSASVFSLLAIAIERHVAIAKVKLYGSDKSCRMLLIG 153
DB 1 GPTVLSLTPLQWFAREGSAFATLSASVFSLLAIAIERHVAIAKVKLYGSDKSCRMMLIG 60

QY 154 ASWLSLVGLGPIILGWNCLGHLACSTVPLPYAKHYVLCVVTIPSIIILAIVALYVRIY 213
DB 61 ASWLSLVGLGPIILGWNCLGHLACSTVPLPYAKHYVLCVVTIPSIIILAIVALYVRIY 120

QY 214 CVRRSSHADMAAPOTLALLKTVTVLVGVFVLCWLPFAFSILLIDYACPVHSCPILYKAHYX 273
DB 121 FVRRSSHADVAGPQTLALLKTVTVLVGVFVLCWLPFAFSILLIDYACPVHSCPILYKAHYX 180

QY 274 FAVSTLNSLL 283
DB 181 FAFATLNSLL 190

RESULT 9
Q5R7A1 PONPY PRELIMINARY; PRT; 382 AA.
AC Q5R7A1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp469M1119.
GN Name=DKFZp469M1119;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; CR860217; CAH92359.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000987; EDG1receptor.
DR InterPro; IPR002277; EDG2_receptor.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR004061; S1P Receptor.
DR PANTHER; PTHR19286; SP5; EDG1receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00642; EDG1RECEPTOR.
DR PRINTS; PR01148; EDG2RECEPTOR.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
SQ SEQUENCE 382 AA; 42773 MW; 6F0841D0E93789CC CRC64;

Query Match 47.4%; Score 856; DB 2; Length 382;
Best Local Similarity 51.4%; Pred. No. 1.3e-50;
Matches 162; Conservative 58; Mismatches 83; Indels 12; Gaps 2;

QY 3 SLYSEYLNPNKQEHYNYT-KETLETQETTSRQVASAFIVLCCAIIVENLLVLIIVARN 61
DB 14 SSVSDYVNDYIIVRHVNYTKLNSADKENSIKLTSVVFILICCFILFNIFVLLTIWKT 73

QY 62 SKFHSAMYLFLGNLAASDLGAVFVANTLLSGSVTLRLTPVOWFAREGSFATLSASVF 121
DB 74 KKFHRPMYFIIGNLSDLLAGVAVYANTLLSGATYKLTQAQWFLREGSMFVALSASF 133

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QY 122 SLAATAIERHVAIAKVKLYGSKDCRMILLIGASWLSILVGLGILGWNCLGHLEACST 181
DB 134 SLAATAIERHVAIAKVKLYGSKDCRMILLIGASWLSILVGLGILGWNCLGHLEACST 193
QY 182 VLPLAKHYVLCVVTTFISILLAIYALVYRIYCVVRS-----SHADMAAPOTLA 230
DB 194 VLPLAKHYVLCVVTTFISILLAIYALVYRIYCVVRS-----SHADMAAPOTLA 253
QY 231 LLKTTVTVLGVFIVCWLPAFSLILLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 290
DB 254 LLKTTVTVLGVFIVCWLPAFSLILLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 313
QY 291 RSRDLRREVLRLPQC 305
DB 314 TNKEMRRAPTRIMSC 328

RESULT 10
ID Q9NYN8 HUMAN PRELIMINARY; PRT; 382 AA.
AC Q9NYN8; Q9BY4;
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE G protein-coupled sphingolipid receptor (Edg1 protein) (Endothelial
DE differentiation, sphingolipid G-protein-coupled receptor, 1).
GN Name=CHEDG1; Synonyms=EDG1; ORFNames=RP4-575N6.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tiyyi G.J. Sr., Wang D. Sr.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marais K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Mkontinya M., Schick M., Eisenstein S.,
RA Neubert P., Katrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]

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RP NUCLEOTIDE SEQUENCE.
RA Grafham D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
DR EMBL; AF233365; AAF43420.1; -; mRNA.
DR EMBL; BC018650; AAH18650.1; -; mRNA.
DR EMBL; CR541786; CAG46585.1; -; mRNA.
DR EMBL; CR542259; CAG47065.1; -; mRNA.
DR EMBL; AL109741; CAI21861.1; -; Genomic DNA.
DR Ensembl; ENSG00000170989; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophingolipid and lysophosphatidic acid . . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000987; EDG1receptor.
DR InterPro; IPR002277; EDG2 receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004061; S1P_receptor.
DR PANTHER; PTHR19266:SF5; EDG1receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00642; EDG1RECEPTOR.
DR PRINTS; PR01148; EDG2RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; UNKNOWN_1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 382 AA; 42811 MW; 0CCE8685A5E1BAD2 CRC64;

Query Match 47.0%; Score 849; DB 2; Length 382;
Best Local Similarity 50.8%; Pred. No. 3.9e-50;
Matches 160; Conservative 59; Mismatches 84; Indels 12; Gaps 2;

QY 3 SLYSEYLNPNKVOEHNYT-KETLETOETTSROVASAFIVILCCAIVVENLLVLIAVARN 61
DB 14 SSVSDYVNDYDIIVRHNYTGKLNISADKENSIKLTSVVFILICCFILLENIFVLLTIWKT 73
QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSAFITLSASVF 121
DB 74 KKFHRPMYFIFGNLSDLLAGVAVTANLLSGATTYKLTTPAQWFLREGSMFVALSASF 133
QY 122 SLAATAIERHVAIAKVKLYGSKDCRMILLIGASWLSILVGLGILGWNCLGHLEACST 181
DB 134 SLAATAIERHVAIAKVKLYGSKDCRMILLIGASWLSILVGLGILGWNCLGHLEACST 193
QY 182 VLPLAKHYVLCVVTTFISILLAIYALVYRIYCVVRS-----SHADMAAPOTLA 230
DB 194 VLPLAKHYVLCVVTTFISILLAIYALVYRIYCVVRS-----SHADMAAPOTLA 253
QY 231 LLKTTVTVLGVFIVCWLPAFSLILLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 290
DB 254 LLKTTVTVLGVFIVCWLPAFSLILLDYPACPVHSCPILYKAHYXFAVSTLSLNPVIYTW 313
QY 291 RSRDLRREVLRLPQC 305
DB 314 TNKEMRRAPTRIMSC 328

RESULT 11
ID EDG1_RAT
AC P48303;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Sphingosine 1-phosphate receptor Edg-1 (Sphingosine 1-phosphate
DE receptor 1) (S1P1).
GN Name=Edg1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.

```

QY	3	SLYSEYNLPNKVOEHYNNYT--KETLETOFTTSRQVASAFIVLTCCCAIVVENLLVLAVARN	61
DB	15	SQVSDYGNVDIIVRRHNYTKMGIVGEKDHGKUTSVVFILICLIIIDENIFVLTTIWT	74
QY	62	SKFHSAMYLPLGNLAASDLIAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASVF	121
DB	75	KKEHRRPMYFIGNLSDLLAGVAYTANLLSGATTYKLTTPAQFLREGSMFVALSASF	134
QY	122	SLIAIAIERHVAIAKVKLYGSDSCRMILLIGASWLISLVGGGLPIGWNCCLGHUEACST	181
DB	135	SLIAIAIERIYITMLKWLHNGSNSSRFLITSACWISLIIIGGLPIGWNCITSSLSGCS	194
QY	182	VLPLYAKHYVLCVVTFTESIITLAIYALYKRYIYCVVR-----SHADMAAPOTLA	230
DB	195	VLPYKHGYILFCTVPTLLLSLIVDYCRYISLVTRSRRLTRKNIISKASRSSEKSLA	254
QY	231	LLKTVITVLGVFTVCMPLPAFSIILLDYACPVHSCPILYKAIYKFAVSTNSILNPIVYT	290
DB	255	LLKTVIIVLSVFACWAPLFIILLDDVGCKAKTCDILYKAEYFLVLAIVLNGSTNPIIYTL	314
QY	291	RSDDLREVLRLPQCWR-PGVGVQGR-RRGCTPGHLLLPURSSS	333
DB	315	TNKEMRRAFRITISCKCPNGDSAGKPKPIIPGMFGRSRKSDNS	359
RESULT 12			
Q4V7F6 RAT			
ID	Q4V7F6	RAT PRELIMINARY; PRT; 383 AA.	
AC	Q4V7F6		
DT	13-SEP-2005	(T-EMBLrel. 31, Created)	
DT	13-SEP-2005	(T-EMBLrel. 31, Last sequence update)	
DT	13-SEP-2005	(T-EMBLrel. 31, Last annotation update)	
DE	DE	Endothelial differentiation sphingolipid G-protein-coupled receptor	
DE	DE	1.	
GN	Name=Edg1;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RP	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Placenta;		
RC	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,		
RA	Schnerch A., Schein J., Jones S.J.M., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).		
RN	[2]		
RN	NUCLEOTIDE SEQUENCE.		
RP	TISSUE=Placenta;		
RC	TISSUE=Placenta;		
RG	NTH MGC Project;		
RL	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
DR	EMBL; BC097938; AAH97938.1; -; mRNA.		
DR	InterPro; IPR000987; EDG1receptor.		


```
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN
[7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Eye, and Mouse;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
[8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN
[9]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AK004591; BAB23393.1; -; mRNA.
DR EMBL; BC049094; AAH49094.1; -; mRNA.
DR EMBL; BC051023; AAH51023.1; -; mRNA.
DR Ensembl; ENSMUSG00000045092; Mus musculus.
DR MGI; MGI:1096355; Edg1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0001525; P:angiogenesis; IDA.
DR GO; GO:0007193; P:G-protein signaling, adenylate cyclase inh. . . ; IDA.
DR GO; GO:0030155; P:regulation of cell adhesion; IDA.
DR InterPro; IPR000987; EDG1receptor.
DR InterPro; IPR002277; EDG2 receptor.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR InterPro; IPR004061; 5TP_receptor.
DR PANTHER; PTHR19266:SF5; EDG1receptor; 1.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00642; EDG1RECEPTOR.
DR PRINTS; PR01148; EDG2RECEPTOR.
DR PRINTS; PR00237; GPCR_RHODOPN.
DR PRINTS; PR01523; 5TPRECEPTOR.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G PROTEIN RECP F1_2; 1.
DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE 382 AA; 42639 MW; 5FE4C9A2BD65C82A CRC64;
SQ
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Query Match 46.8%; Score 845; DB 2; Length 382;
Best Local Similarity 48.7%; Pred. NO. 7.3e-50;
Matches 168; Conservative 60; Mismatches 103; Indels 14; Gaps 4;
QY 3 SLYEYLNPKNVQVHYNT-KETLETQTTTSRQVASAFIVILCCAIIVENLLVLIIVARN 61
DB 14 SSVSDYGNIDYIVRHVNTYTKLNTGAEDHGKIKLTSVVFIICCFIILENIPVLLTIWKT 73
QY 62 SKFHSAMYLFLGNLAASDLLAGVAVNTLLSGVSTLRLTPVQVFAFGSFAFITSASVF 121
DB 74 KKFHRPMYFIGNLALSLLAGVATNLLSGATTYKLTQAQWFLRGSFVALSASFV 133
QY 122 SLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASMLISLVLGGLPILGMCNCLGHLEACST 181
DB 134 SLLAIAIERYITMLKMKLHNGSNSRSRFLISACWVLSILGGLPIMGNCISSLSCST 193
QY 192 VLPLAKHYVLCVVTIFSIILAILAIVLYRYICVRS-----SHADMAAPQTILA 230
DB 194 VLPLVHKHYILFCTTFTVFTLLLSIVLYCRYSLVTRSRRLTFRKNISKASRSSEKSLA 253
QY 231 LLKTTVIVLGVFIVCWLPAFSILLIDYACPVHSCPILYKAHYKFAVSTLNSLNPVIYTW 290
DB 254 LKTVIIVLSVFIACWAEFLILLLDVCKKATCDILYKAEYFVLAVLNSGTNFIYTL 313
QY 291 RSRDLRREVLPLQCR-PGVGVQGR-RRGGTPGHHLPLRSSSS 333
DB 314 TNKEMERAFIRVSCCKPENGDSAGKFKRPIIPGMEFSRSKSDNS 358
RESULT 14
QSBIP0 BOVIN PRELIMINARY; PRT; 382 AA.
ID QSBIP0_BOVIN PRELIMINARY;
AC QSBIP0;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Endothelial differentiation, sphingolipid G-protein-coupled receptor,
DE 1.
GN Name=EDG1;
OS Bos taurus (Bovine) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keefe J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine CDNA
RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RA Harbay G.P., Sonstegard T.S., Van Tassell C.P., Clawson M.L.,
RA Heaton M.P., Keefe J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert CDNA
RT clones.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; BT021184; AAX31366.1; -; mRNA.
DR EMBL; BT021154; AAX31336.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001619; F:lysophospholipid and lysophosphatidic acid . . ; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 06:38:17 ; Search time 24.5 Seconds
(without alignments)
1386.307 Million cell updates/sec

Title: US-10-084-507B-17
Perfect score: 1806
Sequence: 1 MGSLSYSEYLNPNKQEHYNY.....LERGMHMTPTFLEGNTVV 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1625.5	90.0	352	JC1465	probable G protein
2	847	46.9	383	I53870	Edg-1 orphan recep
3	836.5	46.3	381	A35300	G protein-coupled
4	817.5	45.3	362	JC7559	sphingosine 1-phos
5	809	44.8	180	E48909	G protein-coupled
6	769	42.6	378	JC5245	G protein-coupled
7	504	27.9	364	JC5293	lysophosphatidic a
8	352.5	19.5	323	S43850	melanocortin 3 rec
9	349	19.3	362	I65990	G protein-coupled
10	348.5	19.3	360	B46647	melanocortin recep
11	347	19.2	330	A55689	G protein-coupled
12	340.5	18.9	363	S48697	probable G protein
13	338.5	18.7	223	S36636	melanocortin recep
14	338	18.7	330	S40454	G protein-coupled
15	302	16.7	473	A33117	cannabinoid recep
16	300	16.6	325	JC3193	melanocortin recep
17	298.5	16.5	332	A57055	melanocortin recep
18	297	16.4	372	I49008	melanocortin-5 rec
19	296.5	16.4	314	S71420	melanocortin 1 rec
20	296.5	16.4	325	JC5592	melanocortin 5 rec
21	292.5	16.2	325	JN0764	melanocortin recep
22	292.5	16.2	347	S70364	cannabinoid recep
23	288	15.9	472	S17595	cannabinoid recep
24	286	15.8	360	S36750	adenosine receptor
25	285.5	15.8	412	A48978	adenosine receptor
26	285	15.8	317	S45708	MSH receptor - bov
27	283.5	15.7	314	S70005	melanocortin 1 rec
28	283	15.7	410	A48974	adenosine receptor
29	281.5	15.6	320	S18444	G protein-coupled

ALIGNMENTS

RESULT 1

JC1465

probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JC1465

R:Okazaki, H.; Iehizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takawa, Y

Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993

A>Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in t

A:Reference number: JC1465; MUID:93176155; PMID:8382486

A:Accession: JC1465

A:Molecule type: mRNA

A:Residues: 1-352 <OKA>

A:Cross-references: UNIPROT:P47752; UNIPARC:UPI000000007D; GB:AB016931; NID:g3445557; PI

A:Experimental source: aortic smooth muscle

C:Superfamily: G protein-coupled receptor edg-1

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:35-59/Domain: transmembrane #status predicted <TM1>

F:67-95/Domain: transmembrane #status predicted <TM2>

F:110-128/Domain: transmembrane #status predicted <TM3>

F:148-173/Domain: transmembrane #status predicted <TM4>

F:190-210/Domain: transmembrane #status predicted <TM5>

F:234-255/Domain: transmembrane #status predicted <TM6>

F:272-293/Domain: transmembrane #status predicted <TM7>

F:19/Binding site: carboxylate (Asn) (covalent) #status predicted

F:142,145,218,219,329,330,331,332/Binding site: phosphate (Ser) (covalent) #status pred

F:313/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 90.0%; Score 1625.5; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 1.5e-125;
Matches 317; Conservative 13; Mismatches 22; Indels 1; Gaps 1;

QY	1	MGSLSYSEYLNPNKQEHYNYKTLETQETTSRQVASAFIVILCCAIIVVENLLVLIAVAR	60
DB	1	MGGLYSEYLNPEKQEHYNYKTETLDMQETPSRKVASAFIILCCAIIVVENLLVLIAVAR	60
QY	61	NSKPHSAMYLFIGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQMFARGSGAFITLSASV	120
DB	61	NSKPHSAMYLFIGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQMFARGSGAFITLSASV	120
QY	121	PSLLAIATERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPILGWNCILGLEACS	180
DB	121	PSLLAIATERHVAIAKVKLYGSKSCRMILLIGASWLSISLVGLGPILGWNCILGLEACS	180
QY	181	TVLPYAKHYVLGVVTVTFISIIILAIVALYVRIYCVVRRSHADMAAPQTLALKTTIVILG	240
DB	181	TVLPYAKHYVLGVVTVTFISIIILAIVALYVRIYFVRRSHADVAGPQTLALKTTIVILG	240
QY	241	VFIVCWLPAFSILLIDYACPVHSCPILYKHYKFAVSTLNSLNPVYVTVRSRDRLREVL	300
DB	241	VFIIICWLPAFSILLIDSTCPVRCAPVLYKHYKFAVSTLNSLNPVYVTVRSRDRLREVL	300

melanocyte-stimula
melanocyte stimula
A2 adenosine recep
melanocyte-stimula
melanotropin recep
G protein-coupled
alpha-1A-adrenergic
alpha-1A-adrenergic
adrenocorticotropi
adrenocorticotropi
alpha-1-adrenergic
alpha-1A adrenergic
adenosine A2a rece
adrenocorticotropi
5-HT4S receptor -
serotonin 4 recept

30 280 15.5 315 2 S25581
31 279.5 15.5 317 2 T12055
32 279.5 15.5 409 2 I48095
33 273.5 15.1 325 2 I46416
34 272 15.1 317 2 S29204
35 271.5 15.0 412 2 D30341
36 269 14.9 501 2 JH0447
37 269 14.9 572 2 I39369
38 268 14.8 296 2 I52326
39 267 14.8 296 2 JC4046
40 266 14.7 515 2 A40491
41 261 14.5 560 2 A38731
42 259.5 14.4 409 2 S68247
43 257.5 14.3 297 2 C43265
44 256 14.2 387 2 S55550
45 256 14.2 406 2 S55549


```
QY 301 RFLQWRPGVGVQGRRGCTPGHLLPLRSSSSSLRGGMHPT--SPTFLGNTVV 353
Db 305 KMLNC--GVCVQPSGSRP---IMGAEFSTKSDNSHPNKPDEPSPRETIV 353

RESULT 5
E48909
G protein-coupled receptor Gpcrl3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: E48909
R:Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A:Title: Identification, chromosomal location, and genome organization of mammalian G-protein-coupled receptor
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: E48909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-180 <WIL>
A:Cross-references: UNIPROT:P52592; UNIPARC:UPI0000029470; GB:L20334; NID:G438786; PIDN:
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor

Query Match 44.8%; Score 809; DB 2; Length 180;
Best Local Similarity 91.7%; Pred. No. 4.8e-59;
Matches 165; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 62 SKFHSMYFLGNLAASDLLAGVAVNTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 121
Db 1 SKFHSMYFLGNLAASDLLAGVAVNTLLSGSVTLRLTPVQWFAREGSAFITLSASVF 60

QY 122 SLATAIERHVAIAVKLYGSKSCRMILLIGASMLISLVGLGLPLGWNCLHLEACST 181
Db 61 SLATAIERHVAIAVKLYGSKSCRMILLIGASMLISLVGLGLPLGWNCLHLEACST 120

QY 182 VLPLYAKHYVLCVVTIFSIILLAIYALYVRIYCVVRSSHADMAAPQTALLKTTVTLGV 241
Db 121 VLPLYAKHYVLCVVTIFSIILLAIYALYVRIYCVVRSSHADVAGPTALLKTTVTLGV 180

RESULT 6
JC5245
G protein-coupled receptor - human
C:Species: Homo sapiens (man)
C:Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: JC5245
R:Yamaguchi, F.; Tokuda, M.; Hatase, O.; Brenner, S.
Biochem. Biophys. Res. Commun. 227, 608-614, 1996
A:Title: Molecular cloning of the novel human G protein-coupled receptor (GPCR) gene map
A:Reference number: JC5245; MUID:97032811; PMID:8878560
A:Accession: JC5245
A:Molecule type: DNA
A:Residues: 1-378 <YAM>
A:Cross-references: UNIPROT:Q99500; UNIPARC:UPI0000050422; EMBL:X83864; NID:G1770395; PI
C:Comment: This protein transduces hormone and neurotransmitter signals into intracellular
C:Genetics:
A:Gene: edg-3
A:Map position: 9q22.1-q22.2
C:Superfamily: G protein-coupled receptor edg-1
C:Keywords: G protein-coupled receptor

Query Match 42.6%; Score 769; DB 2; Length 378;
Best Local Similarity 47.5%; Pred. No. 1.9e-55;
Matches 162; Conservative 56; Mismatches 101; Indels 22; Gaps 7;

QY 14 VOEHNYT-----KETLETTTSRQVASAFIVLCAIVVENLLVLIARVARNKSHS 66
Db 18 LREHYQVCKLAGRLKEASEGSTLT-----TVLFVLCISFVLENLWLIATWKNKFFN 72

QY 67 AMYFLGNLAASDLLAGVAVNTLLSGSVTLRLTPVQWFAREGSAFITLSASVFLAI 126
Db 73 RMYFFIGNLALCDLAGIAYKNILMSGKTKTSLSPVWFLREGSMFVALGASTCSLLAI 132
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QY 127 AIERHVAIAVKLYGSKSCRMILLIGASMLISLVGLGLPLGWNCLHLEACSTVLPY 186
Db 133 AIERHLTWIKRPYDANKRHRVFLIIGWCLIAFTLGAIPILGWNCLHNLPCDSTILPY 192

QY 187 AKHYVLCVVTIFSIILLAIYALYVRIYCVVRSSHADMA-----APOTLALLKTTVTLGV 242
Db 193 SKKYIAFCISITAILVTIVILYARIYFLVKSSSRKVNHNNSERSMALLRTVWVVSFV 252

QY 243 IVCMPLAFSILLDYACPVHSCPILYKAHYFAVSTLNSLNPVITYTWSRDLRREVLRP 302
Db 253 IACWSPLFILFDVACRVQCPILFKAQWIFVLAVLSAMNPVITYTTLAKEMRRRAFFR- 311

QY 303 LQCVRPVGVQGRRGCTPGHLL-PLRS-SSSLRGGMHMP 341
Db 312 LVC---NCLVRGARGARASPIQALDPSPRSKSSSSNNSSHP 349

RESULT 7
JC5293
lysophosphatidic acid receptor - human
N:Alternate names: Edg2 protein
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: JC5293
R:An, S.; Dickens, M.A.; Bleu, T.; Hallmark, O.G.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 231, 619-622, 1997
A:Title: Molecular cloning of the human Edg2 protein and its identification as a functional
A:Reference number: JC5293; MUID:97224397; PMID:9070858
A:Contents: lung
A:Accession: JC5293
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-364 <ANA>
A:Cross-references: UNIPROT:Q92633; UNIPARC:UPI0000050403; GB:U80811; NID:G1857424; PID
C:Superfamily: G protein-coupled receptor edg-1

Query Match 27.9%; Score 504; DB 2; Length 364;
Best Local Similarity 34.3%; Pred. No. 8.6e-34;
Matches 116; Conservative 71; Mismatches 121; Indels 30; Gaps 9;

QY 18 YNYKETLETTTSRQVASAFIVLCAIVVENLLVLIARVARNKSHSAMYFLGNLAA 77
Db 34 YNRSGKHLATEWNTVSKLVMLGITVCIFIMLANLLVMVAIYVNRFRFPPIYLMANLAA 93

QY 78 SDLLAGVAVNTLLSGSVTLRLTPVQWFAREGSAFITLSASVFSILLATAIERHVAIAKV 137
Db 94 ADFFAGLAYFYLMFTGPNTRLTVSTWLLRQGLDITSLTASVANLLATAIERHITVFRM 153

QY 138 KLYGSKSCRMILLIGASMLISLVGLGLPLGWNCLHLEACSTVLPYAKHYVLCVVTI 197
Db 154 QLHTKMSNRVVVVIWVITWVAIVGAIPSVGVGNICDIENCSNMAPLYSDSY-LVFWAI 212

QY 198 FSII-LLAIALYVRIYCVVR-----SSHADMAAPQ-----TLALLKTTVTLGVFIVC 245
Db 213 FNLVTFVVMVLYAHIFGVYRQRTWRMSRHS--SGPRNRDRMTMSLLKTTVTLVGLAFIC 270

QY 246 WLPAFSILLDYACPVHSCPILYKAHYFAVSTLNSLNPVITYTWSRDLRREVLRPLOC 305
Db 271 WTPGLVLLLDVCCP--QCDVLAYEKFFLLAFAFNSAMNPITYSYRDKEMSAFTFQILCC 328

QY 306 WRPGVGVQGRRGCTPGHLLPLRSSSSSLER-----GMH 339
Db 329 QR-----SENPTGPTSSD-----RSASSLNHTILAGVH 357

RESULT 8
S43850
melanocortin 3 receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C:Accession: S43850; S37153
R:Desarnaud, F.; Labbe, O.; Eggerickx, D.; Vassart, G.; Parmentier, M.
```


A;Residues: 1-330 <IIS>
A;Cross-references: UNIPROT:P46089; UNIPARC:UPI0000001624; GB:L32830; GB:L32831; NID:g60
R;Eggenickx, D.; Denef, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, S.; Vassart, G.; Parmant
Blochem. J. 309, 837-843, 1995
A;Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutively a
A;Reference number: S58521; MUID:95366960; PMID:7639700
A;Accession: S58521
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-330 <EG>
A;Cross-references: UNIPARC:UPI0000001624; GB:X83956; NID:g1061125; PIDN:CAA58787.1; PID
R;Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, H.H.Q.; Tsui, I
Genomics 23, 609-618, 1994
A;Title: Cloning of human genes encoding novel G protein-coupled receptors.
A;Reference number: A55733; MUID:95154831; PMID:7851889
A;Accession: C55733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-292 <MAR>
A;Cross-references: UNIPARC:UPI000016A113; GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:
C;Genetics:
A;Gene: GDB:GPR3
A;Cross-references: GDB:371695; OMIM:600241
A;Map position: lp36.1-lp34.3
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.2%; Score 347; DB 2; Length 330;
Best Local Similarity 33.3%; Pred. No. 5.4e-21;
Matches 96; Conservative 49; Mismatches 107; Indels 36; Gaps 11;

Qy 38 AFIVILCCA---IVVENLILVAVARNKSFHSAMYLFLGNLAASDLLAGVAVP---ANTL 91
Db 42 AMDVVLICISGTVLVCENALVAVITGTPAPRAPMELLVGLSLAVADLLAGLGLVLFHFAVP 101

Qy 92 LSGSVTLRLTPVQWFAREGAFITLSASFVSLAIAIERHVAIAKVKLYGSDKS-CRMLL 150
Db 102 CIGSAEMSLVIV-----GVLWAFATASIGSLAIVDRLYSLXNALTYSETTVTRIV 155

Qy 151 LGASNLISLVGLGPIILGNWCLHLEACSTVPLVYAKHYLCVVTIFSI---LLAIVAL 208
Db 156 MLALVWGAGLGLGLPLVLANWCLDGLTTCGVVYPLSKNHLVLAIAFFMVFIMQLQY 215

Qy 209 YRIVYVVRSSHADMAAPQTLAL-----LKTIVILGVFIVCWLPAFSLILLDY 257
Db 216 ICRIVC-----RHAQOIALQRHLLPASHYVATKKGATLAVLGAFAACWLPPTVYCLIGD 271

Qy 258 ACPVHSCPIYKAHYKFAVSTLNSLNPVIYTWRSRDLRREVLRLPQC 305
Db 272 A---HS-PPLY-TYTLTLPATYNSMINPIIYAFRNQVQK-VLWAVCC 313

RESULT 12
S48697
probable G protein-coupled receptor protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S48697
C;Song, Z.H.; Young III, W.S.; Brownstein, M.J.; Bonner, T.I.
FEBS Lett. 351, 375-379, 1994
A;Title: Molecular cloning of a novel candidate G protein-coupled receptor from rat brain
A;Reference number: S48697; MUID:94364507; PMID:8082799
A;Accession: S48697
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-363 <SON>
A;Cross-references: UNIPROT:P51651; UNIPARC:UPI000012BA34; EMBL:U12006; NID:g551333; PID
C;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor

Query Match 18.9%; Score 340.5; DB 2; Length 363;
Best Local Similarity 34.7%; Pred. No. 2e-20;
Matches 96; Conservative 51; Mismatches 95; Indels 35; Gaps 12;

Qy 41 VILCCA---IVVENLILVAVARNKSFHSAMYLFLGNLAASDLLAGVAVANTLLS---G 94
Db 78 VLLCSGVTVIAGENALVVALLIASTPALRTPMFLVGLSATADLLAGCGLLHFVQYVVP 137

Qy 95 SVTURLTPVQWFAREGAFITLSASFVSLAIAIERHVAIAKVKLYGSDKS-CRMLLIG 153
Db 138 SETVSLLMV-----GFLVASFAASVSLAITVDRLYSLXNALTYYSRRTLGLVHLLA 191

Qy 154 ASWLISLVGLGPIILGNWCLHLEACSTVPLVYAKHYLCVVTIFSIILLAIVALYVRIY 213
Db 192 ATWTVSLGLGLPVLGNWCLADRSVVRPLTSHVAL-LSTSFVFGIMLHLVRI- 249

Qy 214 CVWRSSHAD-----MAAPQTLALK---TVTIVILGVFIVCWLPAFSLIILLDYACPVH 262
Db 250 QVVWRHAHQIALQOHCCLAPPHLAATRKVGVTAAVLGTFCASMLP-PAIV-----CVVG 303

Qy 263 S--CPILYKAHYKFAVSTLNSLNPVIYTWRSRDLRR 297
Db 304 SQEDPAIV-TYATLLPATYNSMINPIIYAFRNQEIQR 339

RESULT 13

S36636

melanocortin receptor 3 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: A48254; S36636

R;Roselli-Rehffuss, L.; Mounjoy, K.G.; Robbins, L.S.; Mortrud, M.T.; Low, M.J.; Tatro, J.

Proc. Natl. Acad. Sci. U.S.A. 90, 8856-8860, 1993

A;Title: Identification of a receptor for gamma melanotropin and other proopiomelanocort

A;Reference number: A48254; MUID:94022273; PMID:8415620

A;Accession: A48254

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-323 <ROS>

A;Cross-references: UNIPROT:P32244; UNIPARC:UPI000012ED4C; EMBL:X70667; NID:g396551; PID

A;Note: submitted to the EMBL Data Library, January 1993

A;Note: in Genbank entry RMC3RA, release 113.0, the source is designated as Rattus ratt

C;Genetics:

A;Gene: MC3-R

C;Superfamily: melanocortin receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.7%; Score 338.5; DB 2; Length 323;

Best Local Similarity 32.1%; Pred. No. 2.6e-20;

Matches 95; Conservative 56; Mismatches 104; Indels 41; Gaps 11;

Qy 41 VILCCAIV--VENLILVAVARNKSFHSAMYLFLGNLAASDLLAGVAVANTLL-----S 93

Db 44 VFLALGIVSLMENTILVILAVVRNGNLHSPMYFFLLSLQADMVLSLSLETIMIVINS 103

Qy 94 GSVTLRLTPVQWFA--EGSAFITLSASFVSLAIAIERHVAIAKVKLYGSDKSCRMILL 151

Db 104 DSLTLEDQFIQHMNDNIFDSMICISLVSATICNLLAIAVDRYVTIFYALRYHSIMTVRKAL- 162

Qy 152 IGASNLISLVGLGPIILGNWCLHLEACSTVPLVY--AKHYVLCVVTIFSIILLAIVALY 209

Db 163 ---SLIVAI-----WVCCG---ICGVMPFIVYSESKMVICULITMFFAFVLLMGTY 207

Qy 210 VRIYCVVR-----SSHADMAAPQTLALAK---TVTIVILGVFIVCWLPAFSLIILLDYA 258

Db 208 IHMFLFARLHVQRIAAALPPADGVAQOQHSCKMGAVTIILLGVFFICWAPFELHLVLIIT 267

Qy 259 CPVHSCPIYKAHY--XFAVSTLNSLNPVIYTWRSRDLRREVLRLPQCWRGVGV 312

Db 268 CPTNFCYCITYAHFTNYLVLMCNVIDPLIYAFRSLEL-RNTFKELLCGCGMNV 322

RESULT 14

S40454

G protein-coupled receptor GPCR21 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S40454
R;Saeki, Y.; Ueno, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, T.
FBS Lett. 336, 317-322, 1993
A;Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which
A;Reference number: S40454; MUID:94085630; PMID:8262253
A;Accession: S40454
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-330 <SAE>
A;Cross-references: UNIPROT:P35413; UNIPARC:UPI0000025C17; GB:D21062; NID:G455487; PIDN:
A;Superfamily: melanocortin receptor
C;Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match 18.7%; Score 338; DB 2; Length 330;
Best Local Similarity 32.3%; Pred. No. 3e-20;
Matches 93; Conservative 50; Mismatches 109; Indels 36; Gaps 10;

Qy 38 AFIVILCCA---IVVENLVLIIVARNKSFHSAVYFLGNLAASDLLAGVAFV---ANTL 91
Db 42 ANDVVLCISGTLVSCENALVAIIIVGTPAPAPMFLVGLSLAVADLLAGLGLVLFHFAADF 101
Qy 92 LSGSVTLRLTPVQWPARGSAFITLSASVFSLLAIAIERHVAIAKVKLYGSDKS-CRMLL 150
Db 102 CIGSPMSMLV-----GVLAFAFTASIGSLAITVDVRLSYLNALTYSETVTRIVV 155
Qy 151 LIGASWLISVLGGPIILGWNLGHLGACSTVLPYAKHYVLCVVTIFSI--ILIAIVAL 208
Db 156 MLALVWVGALGILGVPVLAWNCRDGLTTCGVVYPLSKNHLVLAIAFPFVFGIMQLVQAQ 215
Qy 209 YVRIYCVVRSSHADNAAPQTLAL-----LKTVTIVLGVPIVCMWPAPFSLILIDY 257
Db 216 ICRIVC-----RHAQOIALQRHLLPASHYVATRKGIATLAVVLGAPACWLPFTVYCLGD 271
Qy 258 ACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVLRLQ 305
Db 272 A-----DSRLY-TYLTLPATYNSINPVIIYAFRNQDVQK-VLWAICC 313

RESULT 15
A33117
cannabinoid receptor CB1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A33117; C55879
R;Matsuda, L.A.; Lolait, S.J.; Brownstein, M.J.; Young, A.C.; Bonner, T.I.
Nature 346, 561-564, 1990
A;Title: Structure of a cannabinoid receptor and functional expression of the cloned cDN
A;Reference number: A33117; MUID:90332039; PMID:2165569
A;Accession: A33117
A;Molecule type: mRNA
A;Residues: 1-473 <MAT>
A;Cross-references: UNIPROT:P20272; UNIPARC:UPI000012710C; GB:X55812; NID:g1552375; PIDN:
R;Shire, D.; Carillon, C.; Kaghad, M.; Calandra, B.; Rinaldi-Carmona, M.; Le Fur, G.; Ca
J. Biol. Chem. 270, 3726-3731, 1995
A;Title: An amino-terminal variant of the central cannabinoid receptor resulting from al
A;Reference number: A55879; MUID:95181329; PMID:7876112
A;Accession: C55879
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-107 <SHI>
A;Cross-references: UNIPARC:UPI000017C8D8
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 16.7%; Score 302; DB 2; Length 473;
Best Local Similarity 28.0%; Pred. No. 3.7e-17;
Matches 92; Conservative 58; Mismatches 129; Indels 50; Gaps 8;

Qy 12 NKVQEHYNYTKETLEQ-----TTSRQVASAFI-VILCCAIWVENLLVIAVA 59
Db 84 NKSLSFKNEENIQCGENFMDMECFMILNPSQQLAIAVLSLTGTFTVLENLLVLCVIL 143
Qy 60 RNSKPH-SAMVYLFIGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWPARGSAPFITLSA 118

Db 144 HRSRLRCRPSYHFIFGSLAVADLLGSLVIFVYSFVDFHFVHFRKDSNPVFLFKLGGVTASTFA 203
Qy 119 SVFSLLAIAIERHVAI-----AKVKLYGSDKSCRMILLIGASWLISLVLGGPIILGWNLG 174
Db 204 SVGSLEFLTAIDRYFSIHRPLAYKRIIVTRPKAVVAFCLM---WTIAIVIAVLPLLLGNCK 260
Qy 175 HLEACSTVLPYAKHYVLCVVTIFSIILIAIVALYVRIYCVVRSSHADN----- 223
Db 261 LQSVCSDFPLIDETILMFVIGVTSVLLLFIVAYMYILMKASHAVRMIQRGTQKSI 320
Qy 224 -----AAPQTLALAKTVTLGVFVVCWLPAPFSLILLDYACPVHSCPILYK 269
Db 321 HTSEDKGVQVTRPDQARMDIRLAKTLVLVLIIICWGPLLAIMVYDVFGRKDK---LIK 377
Qy 270 AHYXFA--VSTLNSLLNPVIYTWRSRDLR 296
Db 378 TVFAFCSMLCLLNSTVNPPIIYALRSKDLR 406

Search completed: December 4, 2005, 06:52:57
Job time : 25.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: December 4, 2005, 06:24:31 ; Search time 130 Seconds
(without alignments)
1193.082 Million cell updates/sec

Title: US-10-084-507B-17
Perfect score: 1806
Sequence: 1 MGSLYSEYLNPNKQEHYNY.....LERGHMPTPTFLEGNTVW 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_21:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*
 - 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	99.9	353	2 AAY28288	Predicted
2	1804	99.9	353	2 AAY49904	Aay49904 Human EDG
3	1803	99.8	353	2 AAY28289	Aay28289 EDG-4 ami
4	1787	98.9	353	3 AAB18889	Aabi8889 Amino aci
5	1787	98.9	353	6 ABP59285	Abp59285 Human Edg
6	1787	98.9	353	6 ABP98694	Abp98694 Human End
7	1787	98.9	353	6 ABP08813	Abu08813 Human EDG
8	1787	98.9	353	6 ABP82010	Abp82010 Human sph
9	1787	98.9	353	7 ADC40485	Adc40485 Protein o
10	1787	98.9	353	7 ADD11247	Add11247 Human EDG
11	1787	98.9	353	7 ADD90760	Add90760 Human Edg
12	1787	98.9	353	8 ADH57161	Adh57161 Human end
13	1787	98.9	353	8 ADJ62652	Adj62652 Human end
14	1787	98.9	353	8 ADO29293	Ado29293 Human GPC
15	1787	98.9	353	8 ADO57997	Ado57997 Human EDG
16	1787	98.9	353	8 ADO22422	Ado22422 Human G p
17	1787	98.9	353	8 ADP88359	Adp88359 Human EDG
18	1783	98.7	353	2 AAY49905	Aay49905 Human EDG
19	1783	98.7	353	7 ADD11249	Add11249 Human EDG
20	1755	97.2	353	9 ADU92079	Adu92079 Human end
21	1631.5	90.3	352	3 AAB03966	Aab03966 Murine ED
22	1625.5	90.0	352	2 AAR58712	Aar58712 Fragment
23	1625.5	90.0	352	2 AAW01663	Aaw01663 p(H218).
24	1625.5	90.0	352	2 AAY05492	Aay05492 Human EDG

25	1625.5	90.0	352	2 AAW87790	Aaw87790 Rat H218,
26	1625.5	90.0	352	4 AAU00305	Aau00305 LPA recep
27	1625.5	90.0	352	6 ABU07712	Abu07712 Rat lysop
28	1625.5	90.0	352	6 ABP98696	Abp98696 Rat Endot
29	1625.5	90.0	352	7 ABU61816	Abu61816 Human sph
30	1625.5	90.0	352	8 ADP88361	Adp88361 Rat endot
31	1625.5	90.0	353	7 ADD48927	Add48927 Rat Prote
32	1622.5	89.8	352	6 ABB98695	Abb98695 Murine En
33	1622.5	89.8	352	8 ADO29294	Ado29294 Mouse GPC
34	1509.5	83.6	377	8 ADP29509	Adp29509 Human sec
35	1432	79.3	372	6 ABP59289	Abp59289 Chimeric
36	947	52.4	269	4 ADG15135	Adg15135 Human 7 t
37	947	52.4	274	4 AAM96680	Aam96680 Human rep
38	947	52.4	274	4 ABB96585	Abb96585 Human tes
39	947	52.4	274	4 ADG15162	Adg15162 Human 7 t
40	860.5	47.6	384	6 ABP59281	Abp59281 Chimeric
41	858.5	47.5	384	6 ABP59280	Abp59280 Chimeric
42	858	47.5	391	6 ABP59279	Abp59279 Chimeric
43	854.5	47.3	362	5 ABG75679	Abg75679 Human Edg
44	854.5	47.3	362	8 ADO28787	Ado28787 Arrestin
45	854.5	47.3	362	9 ADX44606	Adx44606 Chimeric

ALIGNMENTS

RESULT 1
AAY28288
ID AAY28288 standard; protein; 353 AA.
XX AAY28288;
XX

DT 12-OCT-1999 (first entry)
XX Predicted polypeptide product from human EDG-4 cDNA.
DE

KW EDG-4; polypeptide; receptor; inflammation; amino acid; G protein;
KW lysolipid; immune response.
XX

OS Homo sapiens.

XX Key Location/Qualifiers
FH Key Location/Qualifiers
FT Misc-difference 273 /label= unknown
FT /note= "encoded by YTT"
XX

PN WO9935259-A1.

PD 15-JUL-1999.

XX 30-DEC-1998; 98WO-CA001195.

PR 30-DEC-1997; 97US-0070185P.

PR 03-APR-1998; 98US-0080610P.

PR 25-NOV-1998; 98US-0109885P.

XX (ALIX) ALLELIX BIOPHARMACEUTICALS INC.

PI Munroe DG, Kamboj R, Peters D, Kooshesh F, Vyas TB, Gupta AK;

DR WPI; 1999-430392/36.

PT New isolated lysolipid/EDG receptor useful in the treatment of asthma and
PT rheumatoid arthritis.

PS Claim 7; Fig 16A; 120pp; English.

CC A novel isolated lysolipid (LL) receptor/EDG receptor (EDG-4). The LL/EDG
CC receptors are involved in an inflammatory response signaling pathway and
CC an apoptotic signaling pathway. They can be used for identifying agonists
CC or antagonists of NF-kB or IL-8 modulated EDG or LL receptors. Agonists
CC can be used for upregulation of an inflammatory process condition or
CC immune response. Antagonists can be used for the downregulation of an

CC inflammatory process condition or immune response. The agonists and
 CC antagonists can also be used for controlling apoptosis in a cell
 CC comprising the L1/EDG receptor. A diagnostic test for aberrant expression
 CC of HEDG-4 can accelerate diagnosis and proper treatment of abnormal
 CC conditions of e.g. the heart, kidney, lung and testis. Specific examples
 CC of conditions in which aberrant expression of HEDG-4 may play a role
 CC include adult respiratory distress, asthma, rheumatoid arthritis, stroke,
 CC neurotrauma, Alzheimer's disease, endotoxic shock, atherosclerosis,
 CC cardiac ischemia, acute pancreatitis, septic shock, psoriasis, acute
 CC cyclosporine nephrotoxicity, HIV/AIDS, myelodysplasia, cirrhosis of the
 CC liver, and early diabetic glomerulopathy, as well as lung damage
 CC following exposure to cigarette smoke, asbestos or silica. HEDG-4
 CC specific antibodies, inhibitors, ligands or their analogs can be used as
 CC bioactive agents to treat inflammation or disease including viral,
 CC bacterial or fungal infections, allergic responses, mechanical injury
 CC associated with trauma, hereditary diseases, lymphoma or carcinoma, or
 CC other conditions which activate the genes of kidney, lung, heart,
 CC lymphoid or tissues of the nervous system

XX Sequence 353 AA;

Query Match 99.9%; Score 1804; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.3e-177;
 Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVASFIVILCCAIWENLLVLIAR 60
 DB 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVASFIVILCCAIWENLLVLIAR 60
 QY 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
 DB 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
 QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPLILGNCLGLEACS 180
 DB 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPLILGNCLGLEACS 180
 QY 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
 DB 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
 QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYKXPAVSTLSLNPVIYTWRSRDLRREV 300
 DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYKXPAVSTLSLNPVIYTWRSRDLRREV 300
 QY 301 RPLQWRPGVGQRRRGGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353
 DB 301 RPLQWRPGVGQRRRGGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353

RESULT 2

AA49904
 ID AA49904 standard; protein; 353 AA.

AC AA49904;

XX 28-JAN-2000 (first entry)

DE Human EDG family H218 protein.

KW Human; EDG family; H218; transmembrane receptor protein; diagnosis;
 KW therapy; bacterial; fungal; viral; infection; HIV; cancer; diabetes;
 KW obesity; anorexia; bulimia; asthma; Parkinson's disease; hypotension;
 KW acute heart failure; hypertension; urinary retention; osteoporosis;
 KW angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy;
 KW benign prostatic hypertrophy; migraine; vomiting; psychotic;
 KW neurological disorder; dyskinesia.

OS Homo sapiens.

PN WO9954351-A1.

XX 28-OCT-1999.

XX 14-APR-1999; 99WO-US008099.
 PF 23-APR-1998; 98US-0082776P.
 XX 03-SEP-1998; 98US-00150650.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX Bergsma DJ, Elshourbagy N, Lane P, Li X, Mooney JL, Tsui P;
 PI WPI; 1999-633972/54.
 XX N-PSDB; AAZ32488.
 DR Novel human transmembrane receptor protein for use in treatment and
 XX diagnosis of disease.
 PT Claim 1; Page 29; 49pp; English.

CC The present sequence is a human EDG family protein designated H218. H218
 CC is used for diagnosing disease or its susceptibility in a subject related
 CC with expression or activity of H218 by determining the presence or
 CC absence of mutation in the polynucleotide encoding H218 in the genome of
 CC the subject and/or analysing for the presence of H218 expression in
 CC sample derived from the subject. It is also used for treating subjects in
 CC need of enhanced activity or inhibition of H218 by administering an
 CC agonist or antagonist respectively. H218 can be used to treat abnormal
 CC conditions such as bacterial, fungal and viral infections, particularly
 CC HIV-1 or 2, cancers, diabetes, obesity, anorexia, bulimia, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
 CC stroke, ulcers, asthma, allergies, benign prostatic hypertrophy,
 CC migraine, vomiting, psychotic, neurological disorders and dyskinesias can
 CC be treated. The H218 polynucleotide can also be used for obtaining
 CC hybridisation probes and primers for isolating full-length clones
 CC encoding H218. The difference in cDNA or genomic sequence between
 CC affected and unaffected individuals is determined to identify mutation
 CC causing the disease. It is also valuable for chromosome identification.
 CC The polypeptide is used for the identification of membrane bound or
 CC soluble receptors through standard receptor binding techniques and also
 CC for structure based design of agonist, antagonist or inhibitor of the
 CC polypeptides

XX Sequence 353 AA;

Query Match 99.9%; Score 1804; DB 2; Length 353;
 Best Local Similarity 99.7%; Pred. No. 1.3e-177;
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVASFIVILCCAIWENLLVLIAR 60
 DB 1 MGSLSYELNPNKVOEHYNYTKETLEQTTSRQVASFIVILCCAIWENLLVLIAR 60
 QY 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
 DB 61 NSKFSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFTLSASV 120
 QY 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPLILGNCLGLEACS 180
 DB 121 FSLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPLILGNCLGLEACS 180
 QY 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
 DB 181 TVPLYAKHYVLCVVTIFSIILAIYALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
 QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYKXPAVSTLSLNPVIYTWRSRDLRREV 300
 DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYKXPAVSTLSLNPVIYTWRSRDLRREV 300
 QY 301 RPLQWRPGVGQRRRGGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353
 DB 301 RPLQWRPGVGQRRRGGTPGHLLPLRSSSSSLERGMHMTPTPTFLEGNVTW 353

	Query Match	99.8%	Score 1803;	DB 2;	Length 353;
	Best Local Similarity	99.4%	Pred. No. 1.7e-177;		
	Matches 351;	Conservative	1;	Mismatches	1; Indels 0; Gaps 0;
Qy	1	MGSLSYSEVLNPKVQEHYNNYKTELTQETTSRQVASAFIVILCCAIWENLLVIAVAR	60		
Db	1	MGSLSYSEVLNPKVQEHYNNYKTELTQETTSRQVASAFIVILCCAIWENLLVIAVAR	60		
Qy	61	NSKPHSAMYLPLGILNLAASDMLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSAV	120		

Query Match 98.9%; Score 1787; DB 3; Length 353;
 Best Local Similarity 99.2%; Pred. No. 7.5e-176;
 Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKQEHYNTKETLETTQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
 DB 1 MGSLYSEYLNPNKQEHYNTKETLETTQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
 DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
 DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLALLKTTIVILG 240
 DB 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLALLKTTIVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
 DB 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 5
 ABP59285
 ID ABP59285 standard; protein; 353 AA.
 AC ABP59285;
 XX
 XX
 DT 10-MAY-2003 (first entry)
 DE Human Edg5 receptor.
 XX Human; Edg5 receptor.
 KW Human; Edg5 receptor.
 XX Homo sapiens.
 OS
 XX WO2003006503-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 10-JUL-2002; 2002WO-US022346.
 XX
 PR 11-JUL-2001; 2001US-00904099.
 XX
 PA (CERE-) CERETEK.
 XX
 PI Shankar G, Munning JN, Spencer JV;
 XX
 DR WPI; 2003-221718/21.
 XX
 PT New chimeric Edg receptor, useful in high-throughput screening assays,
 PT comprises extracellular and transmembrane domains of a first Edg
 PT receptor, and a chimeric intracellular domain of a second Edg receptor.
 XX
 PS Disclosure; Page 19; 71pp; English.
 XX
 CC The present invention relates to Edg receptors (ABP59277-ABP59290). The
 CC Edg receptors, are useful in a high-throughput screening assay to
 CC identify compounds that bind to or modulate the activity of the
 CC polypeptide, in calcium mobilisation assays, binding assays, detection of
 CC CAMP formation, or in reporter gene techniques
 XX
 SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 6; Length 353;

Best Local Similarity 99.2%; Pred. No. 7.5e-176;
 Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLYSEYLNPNKQEHYNTKETLETTQETTSRQVASAFIVILCCAIIVENLLVLIAR 60
 DB 1 MGSLYSEYLNPNKQEHYNTKETLETTQETTSRQVASAFIVILCCAIIVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
 DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180
 DB 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVLGGLPILGNCLGLEACS 180

QY 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLALLKTTIVILG 240
 DB 181 TVLPLYAKHYVLCVVTIFSIILLAI VALYVRIYCVVRSSHADMAAPQTLALLKTTIVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 DB 241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300

QY 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
 DB 301 RPLQWPRGVGVQGRRGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353

RESULT 6
 ABB98694
 ID ABB98694 standard; protein; 353 AA.
 AC ABB98694;
 XX
 XX
 DT 10-JAN-2003 (first entry)
 DE Human Endothelial Differentiation Gene, Edg-5.
 XX
 XX Human; nephrotropic; proliferative glomerular nephritis;
 KW Endothelial Differentiation Gene; Edg-5; IGA nephritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200277642-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 25-MAR-2002; 2002WO-JP002828.
 XX
 PR 26-MAR-2001; 2001JP-00088018.
 PR 06-SEP-2001; 2001JP-00270551.
 XX
 PA (NNSH) NIPPON SHINYAKU CO LTD.
 XX
 PI Takagaki K, Katsuma S, Tsujimoto G;
 XX
 DR WPI; 2003-018956/01.
 DR N-ESDB; ABQ81030.
 XX
 PT Screening drugs for preventing or treating (mesangial) proliferative
 PT glomerular nephritis, based on inhibiting activation of Edg-5 for
 PT particularly Edg-5 receptor antagonists.
 XX
 PS Claim 3; Page 44; 59pp; Japanese.
 XX
 CC The present invention relates to methods for screening for preventives or
 CC remedies for proliferative glomerular nephritis, depending on the
 CC inhibitory effect on Endothelial Differentiation Gene, Edg-5, activation.
 CC The method is especially useful for screening preventives or remedies for
 CC IGA nephritis. The present sequence is human Edg-5, which was used in the
 CC method of the invention
 XX
 SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 6; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKQVQEHYNTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLSYELNPNKQVQEHYNTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60

QY 61 NSKFHSAFMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSFATLSASV 120
DB 61 NSKFHSAFMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSFATLSASV 120

QY 121 FSLLAIAIERHVAIAKVLGYSDKSCRMLLLGASWLSLVLGGLPILGNCGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVLGYSDKSCRMLLLGASWLSLVLGGLPILGNCGLHLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSHADMAAPQTALLKTTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPLLYKAHYKFAVSTLNSLNPVYVTRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPLLYKAHYKFAVSTLNSLNPVYVTRSRDLRREVL 300

QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTY 353
DB 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTY 353

RESULT 7
ID ABU08813
XX ABU08813 standard; protein; 353 AA.
AC ABU08813;
XX

DT 11-AUG-2003 (first entry)
DE Human EDG-5 protein.
XX

KW Human; lymphocyte activation; lymphocyte migration; EDG-5;
KW G-protein coupled receptor; GPCR; lymphocyte; T cell receptor;
KW B cell receptor; CD69; gene therapy; asthma; allergy; autoimmune disease;
KW multiple sclerosis; scleroderma; pernicious anaemia; IDDM;
KW insulin-dependent diabetes mellitus; tissue transplant;
KW Graft-versus-host disease; inflammation; infection.
XX

OS Homo sapiens.
XX
XX US2002155512-A1.
XX
XX 24-OCT-2002.
XX

XX 03-OCT-2001; 2001US-00971228.
XX
XX 18-APR-2001; 2001US-0284763P.
XX
XX (RIGE-) RIGEL PHARM INC.
XX

XX Liao XC, Masuda E, Chu P, Pardo J, Li C, Zhao H, Jiang Y;
XX WPI; 2003-340852/32.
XX

XX Identifying lymphocyte modulator activation/migration, by contacting an
PT EDG G-protein coupled receptor polypeptide or cell having the polypeptide
PT with compound and determining chemical/phenotypic effect of compound on
PT cell.
XX

XX Disclosure; Fig 2; 70pp; English.
PS
XX

XX The invention discloses method for identifying a compound that modulates
CC lymphocyte activation/migration. The method comprises contacting an EDG G
CC -protein coupled receptor (GPCR) family polypeptide, or its fragment or a

CC cell comprising the polypeptide or its fragment with the compound, and
CC determining the chemical/phenotypic effect of the compound upon the cell.
CC Also disclosed are methods for modulating lymphocyte activation or
CC migration in a subject, by administering to the subject a therapeutically
CC effective amount of an identified compound, an EDG polypeptide or a
CC nucleic acid encoding an EDG, or its fragment, and for screening for
CC modulators of lymphocyte activation, by transfecting into lymphocytes a
CC cDNA library, stimulating T or B cell receptors of the lymphocytes,
CC screening for modulation of lymphocyte activation by detecting the level
CC of CD69 cell surface expression and rescuing cDNAs that modulate
CC lymphocyte activation. The method is useful for identifying a compound
CC (such as an antibody, antisense molecule, small organic molecule,
CC sphingolipid or a sphingolipid analogue) that modulates lymphocyte
CC activation or migration. The compounds identified are useful for the
CC treatment (e.g. gene therapy) of diseases such as asthma, allergy,
CC autoimmune diseases such as multiple sclerosis, scleroderma, pernicious
CC anaemia, insulin-dependent diabetes mellitus, conditions related to organ
CC and tissue transplant such as graft-versus-host disease, acute and
CC chronic inflammation, an infection such as viral, fungal, protozoal or
CC bacterial infections and diseases in which activation of immune response
CC and stimulation of lymphocyte migration is desired. The sequence
CC presented is the human EDG-5 protein
XX
XX Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 6; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYELNPNKQVQEHYNTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60
DB 1 MGSLSYELNPNKQVQEHYNTKETLETTQTSRQVASAFIVILCCAIIVVENLLVLIAR 60

QY 61 NSKFHSAFMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSFATLSASV 120
DB 61 NSKFHSAFMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQNFAREGSFATLSASV 120

QY 121 FSLLAIAIERHVAIAKVLGYSDKSCRMLLLGASWLSLVLGGLPILGNCGLHLEACS 180
DB 121 FSLLAIAIERHVAIAKVLGYSDKSCRMLLLGASWLSLVLGGLPILGNCGLHLEACS 180

QY 181 TVPLPYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSHADMAAPQTALLKTTVILG 240
DB 181 TVPLPYAKHYVLCVVTIFSIILAIVALYVRIYCVVRSHADMAAPQTALLKTTVILG 240

QY 241 VFIVCWLPAFSLILLDYACPVHSCPLLYKAHYKFAVSTLNSLNPVYVTRSRDLRREVL 300
DB 241 VFIVCWLPAFSLILLDYACPVHSCPLLYKAHYKFAVSTLNSLNPVYVTRSRDLRREVL 300

QY 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTY 353
DB 301 RPLQWRPGVGVQGRRRGTPGHLLPLRSSSSSLRGHMHMPTSPTFLEGNVTY 353

RESULT 8
ABP82010
ID ABP82010 standard; protein; 353 AA.
XX
XX ABP82010;
AC ABP82010;
XX

DT 04-MAR-2003 (first entry)
DE Human sphingolipid receptor Edg5 protein SEQ ID NO:508.
XX

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW Graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX Homo sapiens.

PN WO200261087-A2.

PD 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US050107.

XX 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burner GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX N-PSDB; AB242860.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82019, which are used in the
CC exemplification of the present invention

XX Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 6; Length 353;

Best Local Similarity 99.2%; Pred. No. 7.5e-176;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCAIVENLLVLIAR 60

DB 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCAIVENLLVLIAR 60

QY 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATILSASV 120

DB 61 NSKPHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATILSASV 120

QY 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGPIGLWNCGLGLEACS 180

DB 121 FSLIAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLISLVLGPIGLWNCGLGLEACS 180

QY 181 TVPLPYAKHYVLCVVTFISIIILALVALYVRIYCVVRSSHADMAAPQTLALKTTVILG 240

XX |||

Db 181 TVPLPYAKHYVLCVVTFISIIILALVALYVRIYCVVRSSHADMAAPQTLALKTTVILG 240

QY 241 VFIVCWLPAPFISILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRRVL 300

XX |||

Db 241 VFIVCWLPAPFISILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRRVL 300

QY 301 RPLOCWRPGVCGVGRRRGTGPHLLPLRSSSLERGMHMETSTPTFLEGNTVV 353

XX |||

Db 301 RPLOCWRPGVCGVGRRRGTGPHLLPLRSSSLERGMHMETSTPTFLEGNTVV 353

RESULT 9

ADC40485

ID ADC40485 standard; protein; 353 AA.

XX AC ADC40485;

XX 18-DEC-2003 (first entry)

XX Protein of human EDG-5.

DE gene expression analysis; collective quantitative analysis;

XX G protein coupled receptor; tyrosine oxidase receptor family;

KW ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis;

KW myocardial infarction; infarct; ischaemic disease; GPCR; human; EDG-5.

XX Homo sapiens.

OS WO2003052096-A1.

XX 26-JUN-2003.

XX 13-DEC-2002; 2002WO-JP013097.

XX 14-DEC-2001; 2001JP-00382053.

XX 21-FEB-2002; 2002JP-00045104.

XX 15-MAY-2002; 2002JP-00140111.

XX 18-NOV-2002; 2002JP-00333769.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Hinuma S, Kobayashi M, Arai T, Fukusumi S, Fujii R, Komatsu H;

PI Matsumura F, Kawamata Y, Ogi K;

XX WPI; 2003-533023/50.

XX N-PSDB; ADC40486.

XX Method for gene expression analysis for treatment of cancers.

XX Disclosure; SEQ ID NO 46; 261pp; Japanese.

XX The invention relates to a novel method for gene expression analysis by
collective quantitative analysis of the expression of a number of genes
to identify those that are promoted or inhibited in a given cell or
tissue. The genes are preferably gene families such as the G protein
coupled receptor family, tyrosine oxidase receptor family, or ion channel
gene family. The methods may be used in treatment of cancers, including
prostate, ovarian, stomach, bladder, breast, and cancer of the
intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used
in the treatment and prevention of atherosclerosis, myocardial
infarction, infarct or ischaemic disease of the brain. This sequence
represents a protein of human EDG-5 of the invention.

XX Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 7; Length 353;

Best Local Similarity 99.2%; Pred. No. 7.5e-176;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCAIVENLLVLIAR 60

DB 1 MGSLSYSLPNKQVQEHYNTKETLETTTSRQVASFIVILCAIVENLLVLIAR 60

QY 61 NSKFSHMYFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
 Db |||||
 QY 61 NSKFSHMYFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
 Db |||||
 QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLILGWNCLGLEACS 180
 Db |||||
 QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLILGWNCLGLEACS 180
 Db |||||
 QY 181 TVLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
 Db |||||
 QY 181 TVLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
 Db |||||
 QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 Db |||||
 QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 Db |||||
 QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
 Db |||||
 QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
 Db |||||

RESULT 10

ADD11247
 ID ADD11247 standard; protein; 353 AA.

AC ADD11247;

DT 01-JAN-2004 (first entry)

XX Human EDG5 protein SEQ ID NO:3.

DE Type II diabetes mellitus; venous thrombosis; pulmonary embolism; EDG5;
 KW EDG5 V286A; antidiabetic; thrombolytic; gene therapy; human.

XX Homo sapiens.

XX WO2003085130-A1.

XX 16-OCT-2003.

XX 07-APR-2003; 2003WO-BF0031569.

XX 09-APR-2002; 2002EP-000007879.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX Kozian D, Kostenis E, Siegler K, Jacobs M, Deleuze J, Ricard S;
 PI Mace S;

DR WPI: 2003-804314/75.

DR N-PSDB; ADD11248.

XX Identifying an increase in risk for Type II diabetes mellitus and/or
 PT venous thrombosis/pulmonary embolism comprises determining in a probe the
 PT presence of amino acid exchange at position 286 from Val to Ala in the
 PT EDG5 protein.

PS Example 2; SEQ ID NO 3; 21pp; English.

XX The present invention describes a method for identifying an increase in
 CC risk for Type II diabetes mellitus and/or venous thrombosis/pulmonary
 CC embolism, comprising determining the presence of amino acid exchange at
 CC position 286 from Val to Ala in the EDG5 protein. Also described: (1) a
 CC method for screening pharmaceuticals useful for treating and/or
 CC preventing type II diabetes and/or venous thrombosis/pulmonary embolism,
 CC where a cell or cell extract is used that contains EDG5 with the amino
 CC acid exchange, or the variation in the nucleotide sequence of EDG5
 CC protein or the EDG5-286-AA; (2) a method for adapting the dosage of the
 CC pharmaceutical described above by testing the human cell for the presence
 CC of EDG5 with the amino acid exchange, or the variation in the nucleotide
 CC sequence of EDG5 protein or the EDG5-286-AA; (3) a method of selecting
 CC patients who will respond type II diabetes and/or venous
 CC thrombosis/pulmonary embolism by testing the probe of the respective

CC patient for the presence of EDG5 with the amino acid exchange, or the
 CC variation in the nucleotide sequence of EDG5 protein or the EDG5-286-AA;
 CC and (4) a test kit for testing the presence of the amino acid exchange,
 CC or the variation in the nucleotide sequence of EDG5 protein or the EDG5-
 CC 286-AA. EDG5 has antidiabetic and thrombolytic activities, and can be
 CC used in gene therapy. The methods are useful for identifying an increase
 CC in risk for type II diabetes mellitus and/or thrombosis/pulmonary
 CC embolism, and for screening pharmaceuticals useful for treating type II
 CC diabetes mellitus and/or venous thrombosis/pulmonary embolism. The
 CC methods are also useful for adapting the dosage of a pharmaceutical
 CC useful for treating the above diseases. The methods are useful for
 CC selecting patients who will respond to the pharmaceutical. The present
 CC sequence represents the human EDG5 protein, which is used in an example
 CC from the present invention.

SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 7; Length 353;

Best Local Similarity 99.2%; Pred. No. 7.5e-176;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSEYLNPNKQEHYNYTKETLETQETTSROVASAFIVILCCAI VVENLLVLIAR 60
 Db |||||

QY 1 MGSLSYSEYLNPNKQEHYNYTKETLETQETTSROVASAFIVILCCAI VVENLLVLIAR 60
 Db |||||

QY 61 NSKFSHMYFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSAPITLSASV 120
 Db |||||

QY 61 NSKFSHMYFLGNLAASDLLAGVAVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
 Db |||||

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLILGWNCLGLEACS 180
 Db |||||

QY 121 FSLLAIAIERHVAIAKVKLYGSDKSCRMILLIGASWLSLVGGPLILGWNCLGLEACS 180
 Db |||||

QY 181 TVLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
 Db |||||

QY 181 TVLPYAKHYVLCVVTIFSIILALVALYVRIYCVVRSSHADMAAPQTALLKTTVIVLG 240
 Db |||||

QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 Db |||||

QY 241 VFIVCWLPAFSLILDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREVL 300
 Db |||||

QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
 Db |||||

QY 301 RPLQWRPGVGVQRRRGTPGHLLPLRSSSSSLRGHMHMPTSPFLEGNVTV 353
 Db |||||

RESULT 11

ADD90760

ID ADD90760 standard; protein; 353 AA.

AC ADD90760;

DT 29-JAN-2004 (first entry)

XX Human Edg5 receptor.

XX receptor; human; Edg5 receptor; gastrointestinal disorder;

XX cardiovascular disorder; hypertension; diabetes; respiratory disorder;

XX asthma; immune disorder; cognitive disorder; memory disorder; obesity;

XX pain; psychotic behaviour; affective disorder; migraine; cancer; AIDS;

XX wound healing; ischaemia-reperfusion injury-related disease.

XX Homo sapiens.

XX US2003130493-A1.

PD 10-JUL-2003.

XX 26-AUG-2002; 2002US-00228762.

XX 22-FEB-1999; 99US-00253998.

XX 16-JUL-1999; 99US-00356315.

PA (BONI/) BONINI J A.
PA (HUN/) HUANG L Y.
PA (BORO/) BOROWSKY B E.
PA (SALO/) SALON J A.
PA (WILS/) WILSON A.
PA (NAGO/) NAGORNY R.
XX
XX
PI Bonini JA, Huang LY, Borowsky BE, Salon JA, Wilson A, Nagorny R;
XX WPI; 2003-829581/77.
XX
XX New mammalian Edg7 receptor proteins and nucleic acids encoding mammalian
PT Edg7 receptors, useful for diagnosing and treating an abnormality
PT associated with the activity of the mammalian Edg7 receptor, e.g. asthma,
PT migraine or cancer.
XX
XX
PS Disclosure; SEQ ID NO 19; 64pp; English.
XX
XX The invention relates to an isolated nucleic acid encoding a mammalian
CC Edg7 receptor. The mammalian Edg7 receptor proteins and nucleic acid
CC encoding the proteins are useful for diagnosing and treating an
CC abnormality associated with the activity of the mammalian Edg7 receptors,
CC e.g. gastrointestinal disorder, a cardiovascular disorder, hypertension,
CC diabetes, respiratory disorder, asthma, immune disorder, cognitive
CC disorder, memory disorder, obesity, pain, psychotic behaviour, affective
CC disorder, migraine, cancer, AIDS, wound healing, or ischaemia-reperfusion
CC injury-related diseases. The nucleic acids and proteins are also useful
CC for developing and designing drugs with higher specificity and fewer side
CC effects. The nucleic acid probes are useful for detecting nucleic acid
CC encoding mammalian Edg7 receptors and antisense oligonucleotides
CC complementary to the nucleic acid sequences. The methods are also useful
CC for identifying agonists and antagonists of Edg7 receptors. The present
CC sequence represents the amino acid sequence of the human Edg5 receptor.
XX
SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 7; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSELYNPNKQEHYNTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
DB 1 MGSLSYSELYNPNKQEHYNTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120

QY 121 FSLIAIAIERHVAITAKVLYGSDKSCRMILLIGASWLISLVGLPILGNWCLGLEACS 180
DB 121 FSLIAIAIERHVAITAKVLYGSDKSCRMILLIGASWLISLVGLPILGNWCLGLEACS 180

QY 181 TVPLYAKHYVLCVVTTFISILLAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
DB 181 TVPLYAKHYVLCVVTTFISILLAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFIWCWLPAPFISILLDYACPVHSCPILYKAHYFAVSTLNSLLNPVIYTWRSRLRREV 300
DB 241 VFIWCWLPAPFISILLDYACPVHSCPILYKAHYFAVSTLNSLLNPVIYTWRSRLRREV 300

QY 301 RPLQCRPGVGQGRRRGTGPHLLPLRSSSSLSERGMHMTSPTFLEGNVTW 353
DB 301 RPLQCRPGVGQGRRRGTGPHLLPLRSSSSLSERGMHMTSPTFLEGNVTW 353

RESULT 12
ADH57161
ID ADH57161 standard; protein; 353 AA.
XX
AC ADH57161;
XX
DT 25-MAR-2004 (first entry)
XX

DE Human endothelial differentiation factor 5 (EDG5) protein SeqID 3.
XX
KW G protein coupled receptor; EDG5; type II diabetes mellitus;
KW venous thrombosis; pulmonary embolism; endothelial differentiation gene;
KW EDG.
XX
OS Homo sapiens.
XX
PN US2003219808-A1.
XX
PD 27-NOV-2003.
XX
PP 21-MAR-2003; 2003US-00393870.
XX
PR 09-AUG-2002; 2002US-0402305P.
XX
PA (KOZI/) KOZIAN D.
PA (KOST/) KOSTENIS E.
PA (SIEG/) SIEGLER K.
PA (JACO/) JACOBS M.
PA (DELE/) DELEUZE J.
PA (RICA/) RICARD S.
PA (MACE/) MACE S.
XX
PI Kozian D, Kostenis E, Siegler K, Jacobs M, Deleuze J, Ricard S;
PI Mace S;
XX
XX WPI; 2004-060183/06.
XX N-PSDB; ADH57162.
XX
PT Identifying an increase in risk for type II diabetes mellitus, venous
PT thrombosis, pulmonary embolism or its combination in subject by
PT determining whether amino acid residue at position 286 of EDG5 protein is
PT alanine.
XX
XX Example 2.4; SEQ ID NO 3; 10pp; English.
XX
XX This invention relates to a novel method for identifying an increase in
CC risk for type II diabetes mellitus, venous thrombosis, pulmonary embolism
CC or a combination thereof. Specifically, it refers to a the endothelial
CC differentiation gene 5 (EDG5) located on chromosome 19p13.2, which
CC encodes a G protein coupled receptor protein. The present invention
CC describes an immunochemically reactive labelled antibody based kit that
CC can be used to identify the Val286Ala variation in the EDG5 protein
CC encoded by a single nucleotide polymorphism. Furthermore, this allele
CC encoding the V286A variant represents a genetic marker that can be useful
CC for preventative treatments of the aforementioned diseases, as well as
CC for adapting drug dosage for patients, for drug screening purposes or for
CC patient selection in phase or clinical studies. This polypeptide sequence
CC is the human EDG5 protein of the invention.
XX
SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 8; Length 353;
Best Local Similarity 99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSLSYSELYNPNKQEHYNTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60
DB 1 MGSLSYSELYNPNKQEHYNTKETLETQETTSRQVASAFIVILCCAIWVENLLVLIAR 60

QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSATITLSASV 120

QY 121 FSLIAIAIERHVAITAKVLYGSDKSCRMILLIGASWLISLVGLPILGNWCLGLEACS 180
DB 121 FSLIAIAIERHVAITAKVLYGSDKSCRMILLIGASWLISLVGLPILGNWCLGLEACS 180

QY 181 TVPLYAKHYVLCVVTTFISILLAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240
DB 181 TVPLYAKHYVLCVVTTFISILLAIYALYVRIYCVVRSSHADMAAPQTLALKTKVTIVLG 240

QY 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
DB 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPTFLEGNTTV 353
DB 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPTFLEGNTTV 353

RESULT 13

ADJ62652
ID ADJ62652 standard; protein; 353 AA.

XX AC ADJ62652;

XX DT 06-MAY-2004 (first entry)

XX DE Human endothelial differentiation gene 5 protein.

XX KW Human; receptor; antisense gene therapy;
KW endothelial differentiation gene 5; EDG5; G protein-coupled receptor;
KW development; wound healing; tissue regeneration; cellular proliferation;
KW apoptosis; cancer; angiogenesis; inflammation;
KW hyperproliferative disorder; developmental disorder.

XX OS Homo sapiens.

XX FN US2004029274-A1.

XX PD 12-FEB-2004.

XX PF 09-AUG-2002; 2002US-00215821.

XX PR 09-AUG-2002; 2002US-00215821.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Wyatt J;

XX DR WPI; 2004-179674/17.

XX DR N-PSDB; ADJ62544.

XX PT New antisense oligonucleotide targeted to nucleic acid encoding
PT endothelial differentiation sphingolipid G-protein-coupled receptor 5,
PT for treating cancer, developmental disorder or a condition arising from
PT aberrant apoptosis.

XX PS Disclosure; Page 31-32; 50pp; English.

XX CC The invention relates to a compound 8-80 nucleobases in length targeted
CC to, and which specifically hybridizes with a nucleic acid molecule
CC encoding endothelial differentiation gene 5 (EDG5, a G protein coupled
CC receptor, involved in development, wound healing, tissue regeneration,
CC cellular proliferation, apoptosis, cancer, angiogenesis and
CC inflammation), and inhibits the expression of EDG5, i.e. is an antisense
CC (AS) oligonucleotide. Also included are a composition comprising the
CC compound and a carrier or diluent and a method for screening an antisense
CC compound (by contacting a preferred target region of a nucleic acid
CC molecule encoding EDG5 with one or more candidate antisense compounds
CC comprising at least an 8-nucleobase portion that is complementary to the
CC preferred target region and selecting for one or more candidate antisense
CC compounds that inhibit the expression of a nucleic acid encoding EDG5).
CC The compound, composition and methods are useful for treating a disease
CC or condition associated with EDG5, such as a hyperproliferative disorder,
CC developmental disorder or a disease or condition arising from aberrant
CC apoptosis. They are also useful in research and diagnostics for
CC modulating the expression of EDG5. Experimental protocols are described
CC but no results are given. The present sequence is the human EDG5 protein.

XX SQ Sequence 353 AA;

Query Match 98.9%; Score 1787; DB 8; Length 353;

Best Local Similarity 99.2%; Pred. No. 7.5e-176;

Matches 350; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MGSLYSEYLNPNKQOEYNYTKETLTQETTSROVASAFIVILCCAI VVENLLVLIAR 60
DB 1 MGSLYSEYLNPNKQOEYNYTKETLTQETTSROVASAFIVILCCAI VVENLLVLIAR 60
QY 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
DB 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120
QY 121 FSLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
DB 121 FSLAIAIERHVAIAKVLYGSDKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
QY 181 TVPLYAKHYVLCVVTIFSIILALVALYVRYICVVRSSHADMAAPOTLALKKTIVTVIG 240
DB 181 TVPLYAKHYVLCVVTIFSIILALVALYVRYICVVRSSHADMAAPOTLALKKTIVTVIG 240
QY 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
DB 241 VFVLCWLPAPFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPIVYTWRSRDLRREVL 300
QY 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPTFLEGNTTV 353
DB 301 RPLQWRPGVGVQGRRRGTGPHHLLPLRSSSSSLRGHMHMPTSPTFLEGNTTV 353

RESULT 14

ADO29293

ID ADO29293 standard; protein; 353 AA.

XX AC ADO29293;

XX DT 29-JUL-2004 (first entry)

XX DE Human GPCR EDG5, SEQ ID NO:394.

XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antidiabetic;
KW CNS; central nervous system; respiratory; antianaemic; antiseborrhoeic;
KW viricide; hepatotropic; antibacterial; antianemic; anorectic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.

XX OS Homo sapiens.

XX PN WO2004040000-A2.

XX PD 13-MAY-2004.

XX PF 09-SEP-2003; 2003WO-US028226.

XX PR 09-SEP-2002; 2002US-0409303P.

XX PR 09-APR-2003; 2003US-0461329P.

XX PA (PRIM-) PRIMAL INC.

XX PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX DR WPI; 2004-390329/36.

XX DR N-PSDB; ADO29865.

XX PT Novel mammalian G protein coupled receptors, useful for identifying

PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 394; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 353 AA;

Query Match	98.9%	Score 1787	DB 8	Length 353
Best Local Similarity	99.2%	Pred. No. 7,5e-176		
Matches 350	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy 1	MGSLYSEYLNPNKVOEHYNYKTELTQETTSRQVASAFIVLCCAIWVENLLVLI	AVAR 60		
Db 1	MGSLYSEYLNPNKVOEHYNYKTELTQETTSRQVASAFIVLCCAIWVENLLVLI	AVAR 60		
Qy 61	NSKFHSAMYLFGNLAAADLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS	AFITLSASV 120		
Db 61	NSKFHSAMYLFGNLAAADLLAGVAFVANTLLSGSVTLRLTPVQWFAREGS	AFITLSASV 120		
Qy 121	FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPIPGWNC	LHLEACS 180		
Db 121	FSLLAIAIERHVAIAKVKLYGSDKSCRMLLIGASWLSLVGLGPIPGWNC	LHLEACS 180		
Qy 181	TVLPLYAKHYVLCVVTIFSIILLATVALYVRIYCVVRSHADMAAPQTL	LAKTKVTIVLG 240		
Db 181	TVLPLYAKHYVLCVVTIFSIILLATVALYVRIYCVVRSHADMAAPQTL	LAKTKVTIVLG 240		
Qy 241	VPVVCWLPAFSLLLDYACPVHSCPILYKAHYXFAVSTLNSLNPIVYTW	SRDLRREVL 300		
Db 241	VPVVCWLPAFSLLLDYACPVHSCPILYKAHYXFAVSTLNSLNPIVYTW	SRDLRREVL 300		
Qy 301	RPLQWRPGVGQRRRGTPGHLLPLRSSSSLSRGMHMTPTFFLEGNTVV	353		
Db 301	RPLQWRPGVGQRRRGTPGHLLPLRSSSSLSRGMHMTPTFFLEGNTVV	353		

RESULT 15

ADO57997

ID ADO57997 standard; protein; 353 AA.

XX

AC ADO57997;
XX 12-AUG-2004 (first entry)
DT Human EDG5 receptor protein.
DE
XX
XX
KW endothelial differentiation sphingolipid; G-protein-coupled receptor 5;
KW EDG5; cardiovascular disease; gastroenterology system; reproductive;
KW peripheral; central nervous system; respiratory; analgesic;
KW antiarrhythmic; antiarteriosclerotic; antiasthmatic; antibacterial;
KW antifertility; antiinflammatory; antiparkinsonian; antiulcer; cardiac;
KW cerebroprotective; dermatological; gynecological; neuroprotective;
KW nootropic; vasotropic; virucide; human.
XX
OS Homo sapiens.
XX
XX WO2004044587-A2.
XX 27-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-EP012122.
XX
XX 13-NOV-2002; 2002EP-00025098.
XX (PARB) BAYER HEALTHCARE AG.
XX
XX Golz S, Brueggemeier U, Summer H;
XX WPI; 2004-449580/42.
XX N-PSDB; ADO57996.
XX
PT Screening for therapeutic agents, useful for treating e.g. respiratory
PT disease, comprises contacting a test compound with endothelial
PT differentiation sphingolipid G-protein-coupled receptor 5 polypeptide and
PT detecting binding.
XX
XX Disclosure; SEQ ID NO 2; 119pp; English.
XX
CC The invention relates to a novel method for screening for therapeutic
CC agents. The method comprises contacting a test compound with an
CC endothelial differentiation sphingolipid G-protein-coupled receptor 5
CC (EDG5) polypeptide or polynucleotide and detecting binding of the test
CC compound, or determining EDG5 polypeptide activity at a certain test
CC compound concentration or in the absence of the test compound and at a
CC different concentration of the test compound. The invention further
CC comprises: diagnosing diseases such as a cardiovascular diseases,
CC disorders of the gastroenterology system, reproductive diseases,
CC disorders of the peripheral and central nervous system, and respiratory
CC diseases in a mammal. The invention also comprises a pharmaceutical
CC composition for the treatment of the diseases above comprising an EDG5
CC polypeptide, an EDG5 polynucleotide, or a therapeutic agent which binds
CC to an EDG5 polypeptide or which regulates the EDG5 polypeptide activity
CC such as a small molecule, an RNA molecule, an antisense oligonucleotide,
CC a polypeptide, an antibody, or a ribozyme, and preparation of a
CC pharmaceutical composition useful for treating the above-defined
CC diseases. The compositions have the following activities: analgesic,
CC antiarrhythmic, antiarteriosclerotic, antiasthmatic, antibacterial,
CC antifertility, antiinflammatory, antiparkinsonian, antiulcer, cardiac,
CC cerebroprotective, dermatological, gynecological, neuroprotective,
CC nootropic, vasotropic, and virucide. The regulators of EDG5 are useful
CC for preparing a pharmaceutical composition for treating disease such as
CC cardiovascular diseases, disorders of the gastroenterology system,
CC reproductive diseases, disorders of the peripheral and central nervous
CC system, and respiratory diseases in a mammal. They are also useful for
CC the regulation of EDG5 activity in a mammal having the disease.
CC Cardiovascular disease includes heart failure, myocardial infarction,
CC ischaemia, arrhythmias, and atherosclerosis. Examples of disorders of the
CC gastroenterology system are dysphagia, Barrett's metaplasia, stress
CC gastritis, gastric ulcers, and chronic pancreatitis. Examples of
CC reproduction disorders are syphilis, genital warts, impotence, vaginitis,
CC dysmenorrhoea, and infertility. Disorders of the peripheral and central
CC nervous system include Parkinson's disease, dementia, multiple sclerosis,
CC stroke, and Alzheimer's disease. Respiratory diseases can be asthma or

CC chronic obstructive pulmonary disease. The nucleotide sequences encoding
CC EDG5 are useful as hybridization probes, in constructing oligomers for
CC PCR, for chromosome and gene mapping, in the recombinant production of
CC EDG5, in generating antisense DNA or RNA and in molecular biology
CC techniques that have not yet been developed. EDG5 polypeptides are useful
CC for immunising a mammal to produce polyclonal antibodies and for
CC diagnostic purposes. This sequence represents the human EDG5 receptor
CC protein of the invention.
XX
XX

SQ	Sequence 353 AA;
Query Match	98.9%; Score 1787; DB 8; Length 353;
Best Local Similarity	99.2%; Pred. No. 7.5e-176;
Matches 350; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
QY	1 MGSLYSEYLNPNKQEHYNYTKETLETTQETTSRQVASAFIVILCCAIYVENLLVLIIVAR 60
DB	1 MGSLYSEYLNPNKQEHYNYTKETLETTQETTSRQVASAFIVILCCAIYVENLLVLIIVAR 60
QY	61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
DB	61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSAFITLSASV 120
QY	121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
DB	121 FSLAIAIERHVAIAKVKLYGSKSCRMILLIGASWLSLVLGGLPILGNWCLGLEACS 180
QY	181 TVLPLYAKHYVLCVVTIFSIILLAIYALYVRIYCVRRSHADMAAPOTLALKTTIVILG 240
DB	181 TVLPLYAKHYVLCVVTIFSIILLAIYALYVRIYCVRRSHADMAAPOTLALKTTIVILG 240
QY	241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300
DB	241 VFIVCWLPAFSLILLDYACPVHSCPILYKAHYXFAVSTLNSLLNPVIYTWRSRDLRREV 300
QY	301 RPLQWRPQGVQGRRRGTPGHLLPLRSSSLERGMHMTPTPTFLEGNTVV 353
DB	301 RPLQWRPQGVQGRRRGTPGHLLPLRSSSLERGMHMTPTPTFLEGNTVV 353

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